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(54) Title: VIRULENCE GENES, PROTEINS, AND THEIR USE

(57) Abstract: Virulence genes of *Yersinia* species are identified that encode products which may be of use in therapy or diagnosis. The genes are identified as SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 57, 58 and 64.

VIRULENCE GENES, PROTEINS, AND THEIR USE

Field of the Invention

This invention relates to virulence genes and proteins, and their use. More particularly, it relates to genes and proteins/peptides obtained from *Yersinia pseudotuberculosis*, and their use in therapy and in screening for drugs.

Background of the Invention

Yersinia pseudotuberculosis is an organism that is implicated in gastroenteritis, terminal ileitis and mesenteric adenitis in humans and Yersiniosis in livestock. It is desirable to provide a means for treating or preventing conditions caused by *Yersinia pseudotuberculosis*, e.g. by immunisation.

Summary of the Invention

The present invention is based on the discovery of virulence genes in *Yersinia* species, in particular, *Yersinia pestis* and *Yersinia pseudotuberculosis*.

According to a first aspect of the invention, a peptide of the invention is encoded by a gene comprising any of the nucleotide sequences identified herein as SEQ ID NOS. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 57, 58 and 64, or a homologue thereof in a Gram-negative bacterium having at least 60% sequence similarity or identity at the peptide or nucleotide level, or a functional fragment thereof, for therapeutic or diagnostic use.

The peptide has many therapeutic uses for treating *Yersinia* infections, including use in vaccines for prophylactic application.

According to a second aspect of the invention, a polynucleotide encoding a peptide defined above, is also useful for therapy or diagnosis.

According to a third aspect of the invention, a gene that encodes the peptide is utilised to prepare an attenuated microorganism. The attenuated microorganism has a mutation that disrupts the expression of a gene identified herein, to provide a strain that lacks virulence. This microorganism will also have use in therapy and diagnosis.

According to a fourth aspect of the invention, a peptide, gene or attenuated microorganism of the invention is used in the preparation of a medicament for the treatment or prevention of a condition associated with infection by *Yersinia* or Gram-negative bacteria, e.g. gastroenteritis.

According to a fifth aspect of the invention, a vaccine comprises a peptide of the invention, in a suitable diluent, excipient or pharmacologically acceptable buffer. The vaccine is used in therapy to treat or prevent infection by *Yersinia* or Gram-negative bacteria.

According to a sixth aspect of the invention, an antibody is raised against a peptide of the invention. The antibody can be used in immunotherapy to treat infection.

According to a seventh aspect of the invention, a peptide, polynucleotide or microorganism of the invention is used in an assay to screen for potential antimicrobial drugs.

Description of the Invention

The present invention is based on the discovery of genes encoding peptides which are implicated in virulence. A peptide and gene of the invention is therefore useful for the preparation of therapeutic agents to treat infection. It should be understood that references to therapy also include preventative treatments, e.g. vaccination. Furthermore, while the products of the invention are intended primarily for treatment of infections in human patients, veterinary applications are also considered to be within the scope of the invention.

The present invention is described with reference to *Yersinia pseudotuberculosis*. However, all the *Yersinia* strains, and many other Gram-negative bacterial strains, are likely to include related peptides or proteins having amino acid sequence identity or similarity to those identified herein. Organisms likely to contain the peptide include, but are not limited to the genera *Salmonella*, *Enterobacter*, *Klebsiella*, *Shigella* and *Yersinia*.

In a preferred embodiment, the peptides comprise the *Yersinia pseudotuberculosis* amino acid sequence that corresponds to that disclosed herein for *Yersinia pestis*.

Preferably, the peptides that may be useful in the various aspects of the invention have greater than a 60% similarity with the peptides identified herein. More preferably, the peptides have greater than 80% sequence similarity. Most preferably, the peptides have greater than 90% sequence similarity, e.g. 95% similarity. With regard to the polynucleotide sequences identified herein, related polynucleotides that may be useful in the various aspects of the invention have greater than 60% identity with the sequences identified herein. More preferably, the polynucleotide sequences have greater than 80% sequence identity. Most preferably, the polynucleotide sequences have greater than 90% sequence identity, e.g. 95% identity.

The terms "similarity" and "identity" are known in the art. The use of the term "identity" refers to a sequence comparison based on identical matches between correspondingly identical positions in the sequences being compared. The term "similarity" refers to a comparison between amino acid sequences, and takes into

account not only identical amino acids in corresponding positions, but also functionally similar amino acids in corresponding positions. Thus similarity between polypeptide sequences indicates functional similarity, in addition to sequence similarity.

Levels of identity between gene sequences and levels of identity or similarity
5 between amino acid sequences can be calculated using known methods. In relation to the present invention, publicly available computer based methods for determining identity and similarity include the BLASTP, BLASTN and FASTA (Atschul *et al.*, J. Molec. Biol., 1990; 215:403-410), the BLASTX program available from NCBI, and the Gap program from Genetics Computer Group, Madison WI. The levels of similarity and
10 identity provided herein, were obtained using the Gap program, with a Gap penalty of 12 and a Gap length penalty of 4 for determining the amino acid sequence comparisons, and a Gap penalty of 50 and a Gap length penalty of 3 for the polynucleotide sequence comparisons.

Having characterised a gene according to the invention, it is possible to use the
15 gene sequence to search for related genes or peptides in other microorganisms. This may be carried out by searching in existing databases, e.g. EMBL or GenBank.

Peptides or proteins according to the invention may be purified and isolated by methods known in the art. In particular, having identified a gene sequence, it will be possible to use recombinant techniques to express the gene in a suitable host. Active
20 fragments and related molecules can be identified and may be useful in therapy. For example, a peptide or its active fragment may be used as an antigenic determinant in a vaccine, to elicit an immune response. They may also be used in the preparation of antibodies, for passive immunisation, or diagnostic applications. Suitable antibodies include monoclonal antibodies, or fragments thereof, including single-chain Fv
25 fragments. Methods for the preparation of antibodies will be apparent to those skilled in the art.

Active fragments are those that retain a biological function of the peptide or which generate antibodies that are specific for that peptide. For example, when used to elicit an immune response, the fragment will be of sufficient size, such that antibodies
30 generated from the fragment will discriminate between that peptide and other peptides of the bacterial microorganism. Typically, the fragment will be at least 30 nucleotides (10 amino acids) in size, preferably 60 nucleotides (20 amino acids) and most preferably greater than 90 nucleotides (30 amino acids) in size.

It should also be understood, that in addition to related molecules from other
35 microorganisms, the invention encompasses modifications made to the peptide and

polynucleotide identified herein which do not significantly alter its biological role. It will be apparent to the skilled person that the degeneracy of the genetic code can result in polynucleotides with minor base changes from those specified herein, but which nevertheless encode the same peptide. Complementary polynucleotides are also
5 within the invention. Conservative replacements at the amino acid level are also envisaged, i.e. different acidic or basic amino acids may be substituted without substantial loss of function.

Included within the scope of the claimed invention are molecules that comprise a polynucleotide which hybridizes under stringent hybridization conditions to a portion
10 of a polynucleotide of the invention. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

15 By a "polynucleotide which hybridizes to a portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridization to at least 15 nucleotide bases, and more preferably at least 20 nucleotide bases, still more preferably at least 30 nucleotide bases, and even more preferably 30-70 (e.g. 50) nucleotide bases of the reference polynucleotide.

20 The preparation of vaccines based on attenuated microorganisms is known to those skilled in the art. Vaccine compositions can be formulated with suitable carriers or adjuvants, e.g. alum, as necessary or desired, to provide effective immunisation against infection. The preparation of vaccine formulations will be apparent to the skilled person. The attenuated microorganisms may be prepared with a mutation that disrupts
25 the expression of a gene identified herein. The skilled person will be aware of methods for disrupting expression of particular genes. Techniques that may be used include insertional inactivation or gene deletion techniques. Attenuated microorganisms according to the invention may also comprise additional mutations in other genes, for example in a gene required for growth of the microorganism, e.g. an *aro* mutation.

30 Attenuated microorganisms may also be used as carrier systems for the delivery of heterologous antigens, therapeutic proteins or nucleic acids (DNA or RNA). In this embodiment, the attenuated microorganisms are used to deliver a heterologous antigen, protein or nucleic acid to a particular site *in vivo*. Introduction of a heterologous antigen, peptide or nucleic acid into an attenuated microorganism can be
35 carried out by conventional techniques, including the use of recombinant constructs,

e.g. vectors, which comprise polynucleotides that express the heterologous antigen or therapeutic protein, and also include a suitable promoter sequence. Alternatively, the gene that encodes the heterologous antigen or protein may be incorporated into the genome of the organism and an endogenous promoter used to control expression.

5 More generally, and as is well known to those skilled in the art, a suitable amount of an active component of the invention can be selected, for therapeutic use, as can suitable carriers or excipients, and routes of administration. These factors will be chosen or determined according to known criteria such as the nature/severity of the condition to be treated, the type and/or health of the subject etc.

10 In a separate embodiment, the products of the invention may be used in screening assays for the identification of potential antimicrobial drugs or for the detection for virulence. Routine screening assays are known to those skilled in the art, and can be adapted using the products of the invention in the appropriate way. For example, the products of the invention may be used as the target for a potential drug,
15 with the ability of the drug to inactivate or bind to the target indicating its potential antimicrobial activity.

The various products of the invention may also be used in veterinary applications.

The following is a summary of the experimental procedure used to identify the
20 virulence genes. The full experimental procedure and results have now been published in Karlyshev *et al.*, Infection and Immunity, 2001; 69(12): 7810-7819.

The virulence genes of the invention were identified using a modified version of the signature-tagged mutagenesis (STM) method (Hensel *et al.*, Science, 1995; 269: 400-403), to screen a *Yersinia pseudotuberculosis* mutant bank for attenuated mutants,
25 in a murine model of Yersiniosis infection. Bacteria containing a transposon insertion within a virulence gene failed to be recovered from mice inoculated with a mixed population of mutants.

The transposons used in the method contained DNA tags that were amplified using biotinylated primers and hybridised to high-density oligonucleotide arrays
30 containing DNA complementary to the tags. Comparison of the hybridisation signals from input pools and output pools identified mutants whose relative abundance was significantly reduced in the output pool.

The sequence data from the transposon insertion regions was then compared to the complete *Yersinia pestis* C092 genome sequence.

35 Bacterial strains and growth conditions:

Y. pseudotuberculosis YPIII pIB1 strain (Rosquist *et al.*, Nature, 1988; 334: 522-525) was maintained in Luria Broth (LB) and LB agar containing nalidixic acid (40 µg ml⁻¹). *E. coli* XL2 Blue MRF' (Stratagene), used in cloning experiments, were grown overnight at 37°C on LB agar plates. For selection, agar plates were supplemented with the antibiotics kanamycin (50 µg ml⁻¹), ampicillin (100 µg ml⁻¹), tetracycline (10 µg ml⁻¹) or nalidixic acid. *E. coli* CC118(λ*pir*) (Herrero *et al.*, J. Bacteriol, 1990; 172: 6557-6567) was used as a host strain for maintenance of the *pir*-dependent pUT mini-Tn5Km2 vector (de Lorenzo *et al.*, J. Bacteriol., 1990; 172: 6568-6572) in cloning experiments. The helper strain *E. coli* S17/pNJ5000 was maintained as described in Grinter *et al.*, Gene, 1983; 21: 133-143.

Construction of double-tagged mini-Tn5 transposon mutants:

Tag-sequences were chosen from those that had been shown to work well in similar experiments with *Saccharomyces cerevisiae* (Winzeler *et al.*, Science, 1999; 285: 901-906). The sequences of the 192 PCR primers (primer A and primer B) and the preparation of plasmids carrying tagged mini-Tn5 transposons are shown in Karlyshev *et al.*, 2001, *supra*.

Conjugation:

Initial triple mating experiments of *E. coli* CC118 (λ*pir*) donor strain, transformed with the plasmids carrying tagged mini-Tn5, and *Y. pseudotuberculosis* using a helper strain *E. coli* S17/pNJ5000 (Grinter *et al.*, 1984, *supra*) were performed as described in Oyston *et al.*, Microbiology, 1996; 142: 1847-1853. Direct mating experiments (without a helper strain) using *E. coli* 19851 *pir*⁺ as the donor strain were performed as described in Metcalf *et al.*, Plasmid, 1996; 35: 1-13. Exconjugants were selected for kanamycin and nalidixic acid resistance. Both the recipient strain, YPIII pIB1, and the exconjugants were checked for the presence of the virulence plasmid using Congo red magnesium oxalate (CRMOX) plates (Riley *et al.*, J. Clin. Microbiol., 1989; 27: 213-214. All attenuated transposon derivatives grew as predominantly small red colonies, confirming that they retained the virulence plasmid.

Tag sequence detection:

Genomic DNA was extracted and the tags identified according to the protocol in Karlyshev *et al.*, 2001, *supra*.

In vivo experiments:

Three input pools containing 60, 40 and 33 transposon mutants respectively, were constructed and stored at -70°C. Aliquots (0.1 ml) containing approximately 10⁷ cfu were inoculated into 10 ml LB and incubated with shaking overnight at 30°C. The

overnight culture (2 ml) was used to inoculate 20 ml of fresh pre-warmed LB and further incubated at 37°C for 3 hours with shaking.

Genomic DNA was isolated from approximately 10^8 cells and stored (input pool). Bacteria were pelleted at 3,000 x g and diluted in Phosphate buffered saline (PBS) for infection and viable count determination. Pairs of eight-week-old female Balb/c mice were challenged intravenously (iv) via the tail vein with 10^5 or 5×10^5 cfu. After 3 days, the surviving mice were culled, spleens were removed and homogenized in 3 ml of LB using a stomacher (Seward Medical Ltd) on maximum setting for 5 minutes. Dilutions of the extracts were plated on LB agar containing kanamycin and nalidixic acid. Plates containing approximately 10^4 colonies were washed with saline, mixed and aliquots were taken for making lysates (for PCR) or for total DNA preparation. Genomic DNA recovered from the spleens were the output pools.

Mutants with reduced survival *in vivo* were visualised by comparing the scanned images from arrays that had been hybridized with tags amplified from the input pools with images obtained from two independent output pools.

The input and output pools of the mutants were compared by hybridizing the labeled amplified tags to high-density oligonucleotide arrays (Affymetrix) containing complementary DNA sequences. The hybridization patterns were found to be reproducible. Mutants that showed reduced signals in the output pool for both tags in duplicate mice were selected for further analysis.

Characterization of attenuated mutants and identification of the transposon insertion sequences:

Approximately 5% out of 603 exconjugants exhibited a statistically valid reduction of signal intensity. Transposon insertion sites in the selected mutants were sequenced using a single primer PCR sequencing procedure (Karlyshev *et al.*, BioTechniques, 2000; 28: 1078-1082). The results are summarized in Tables 1 and 2. The *Y. pestis* genome sequence database (http://www.sanger.ac.uk/Projects/Y_pestis/) was used for identification of the corresponding genes in that pathogen; almost 100% identity of the *Y. pseudotuberculosis* sequences to the *Y. pestis* DNA sequences implies similarity in their function. The YPO number is the accession number that is used to identify the gene in the *Y. pestis* genome sequence database. The SEQ ID NOS. 1-58 and 64 are the *Yersinia pestis* sequences. SEQ ID NOS. 35, 56, 57 and 58 are genes in *Y. pestis* that appear to be non-functional in that they appear to contain many mutations in the gene sequence that disrupt the expression of an amino acid product. However, the orthologue (homologue) in *Y. pseudotuberculosis*.

is expected to be functional. The reference to "nrdb" refers the non-redundant amino acid database (www.blast.genome.ad.jp). Any orthologue found in this database is indicated in the columns to the right of the nrdb value.

Certain gene sequences had no orthologue in *Y. pestis*. These genes are identified herein by the mutant number 5D12, 5H10, 5B12, 1A9-1 and 1C9. The sequence provided herein for these mutants is not the complete gene sequence but is the flanking sequence of the transposon insertion site in *Yersinia pseudotuberculosis*. This sequence may not be part of the virulence gene but may be an upstream regulatory site. The flanking sequence is used to identify a suitable site for mutation that will result in a loss of virulence in the microorganism. Accordingly, mutant microorganisms can be prepared which have an attenuating mutation within the sequence identified herein.

In addition to the preparation of attenuated microorganisms, the encoded products of the genes identified herein are suitable as targets for immunotherapy or as immunogenic components of vaccines. In this context, the products identified by the references 5E4, 2G8, 5G6, 1D12, 5G7, 1A9, 4H2, 3G1, 5A5, 3F10, 2B3, 1H6, 2G5, 3G6, 2G10, 1H9, 4F4 and 4G11, are all preferred as they are located on the outer or inner membrane, or are extracellular proteins, shown in Table 3. In Table 3, IM, PP, OM and EC denote inner membrane, periplasmic, outer membrane and extracellular, respectively.

Table 1.

Mutant	SEQ ID NO.	<i>In vivo</i> CI	<i>In vitro</i> CI	Similarity, <i>Y. pestis</i> (%)	<i>Y. pestis</i> ORF	Similarity, nrdb (%)	Product	Microorganism
4H9	1	0.03	0.06	97	YPO0054	85	glycosyltransferase	<i>S. marcescens</i>
2B3	3	1.02	0.85	94	YPO0337	NS	-	-
5E4	5	NT	NT	99	YPO0702	46	putative lipoprotein	<i>Mycobacterium tuberculosis</i>
30.	7	0.48	0.31	98	YPO1108	91	citrate synthase	<i>S. typhimurium</i>
2G8	9	0.53	1.34	96	YPO1174	39	Adhesin	<i>E. coli</i>
3C10	11	0.055	1.02	98	YPO1186	66	hypothetical	<i>E. coli</i>
3H10	13	0.08	0.07	97	YPO1382 (promoter region)	43	LpsA, glycosyltransferase	<i>Pasteurella haemolytica</i>
5G6	15	0.021	0.88	95	YPO1987	NS	-	-
1D12	17	0.084	1.34	97	YPO1994	NS	-	-
1H10	19	NT	NT	98	YPO2174	62	UDP-glucose 6- dehydrogenase	<i>Rhizobium meliloti</i>
4H10	21	0.0036	1.95	96	YPO2287a	65	ABC-transporter	<i>Methanococcus jannaschii</i>
5G7	23	0.25	1.09	98	YPO2440	82	iron(III) dicitrate ATP-binding protein	<i>Haemophilus influenzae</i>
1A9	25	NT	NT	100	YPO2532	NS	-	-
4H2	27	NT	NT	98	YPO2712	77	RseA, negative regulator of RpoE (sigma 24)	<i>E. coli</i>
5E6	56	0.27	1.24	97	YPO3004	47	Pro-dipeptidase	<i>B. subtilis</i>
1D2	29	0.43	0.08	96	YPO3099	100	ManC, mannose-1-P guanylyltransferase	<i>Y. pseudotuberculosis</i>
3G2	57	0.13	NT	98	YPO3100	100	Fcl, fucose synthetase	<i>Y. pseudotuberculosis</i>
1B3	31	0.29	0.98	90	YPO3104	100	O-antigen polymerase	<i>Y. pseudotuberculosis</i>
1D9	58	NT	0.07	98	YPO3114	100	DdhB, CDP-D- glucose-dehydratase	<i>Y. pseudotuberculosis</i>
3F3	33	0.04	0.44	95	YPO3116	100	AscD, ascarilose biosynthesis	<i>Y. pseudotuberculosis</i>
3G1	35	0.21	1.25	97	YPO3144	89	MdIB, Multi-drug resistance protein	<i>E. coli</i>
5A5	36	0.44	1.16	98	YPO3572	88	hypothetical transcription factor	<i>E. coli</i>

1G6	38	NT	NT	97	YPO3657 (intergenic)	NS	Unknown	-
3F10	40	0.017	0.46	99	YPO3834	87	PldA, phospholipase A	<i>E. coli</i>
1G6-1	42	NT	0.41	96	YPO3965	47	VirA, His kinase	<i>Agrobacterium tumefaciens</i>
5D12	59	0.003	0.98	NS	-	80	Wzx	<i>S. typhimurium</i>
5H10	60	NT	NT	NS	-	70	phage-related transcription activator	<i>Xylella fastidiosa</i>
5B12	61	0.89	1.32	NS	-	59	hypothetical	<i>phage HP1</i>
1A9-1	62	NT	NT	NS	-	NS	Unknown	-
1C9	63	NT	0.36	NS	-	NS	Unknown	-
1G6a	64	NT	NT	100	YPO03657a	-	YhdT	<i>E. coli</i>

Table 2

Mutant	SEQ ID NO.	Orthologue in <i>Y. Pestis</i>
2G5	44	YPO1485
3G6	46	YPO2503
2G10	48	YPO1483
1H9	50	YPO1696
4F4	54	YPO0036
4G11	52	YPO3010

Table 3

Mutant	Orthologue in <i>Y. pestis</i>	Orthologue in nrdb	Gene name	YP product size, aa	subcellular location ¹
1H6	YPO3965	VirA, <i>Agrobacterium tumefaciens</i> , 9e-30	<i>virA</i>	851	IM
3F10	YPO3834	PldA, <i>S. typhimurium</i> , e-127	<i>pldA</i>	292	OM
2G8	YPO1174	low score similarities to C-term domains of various OM proteins	-	309	OM
5G7	YPO2440	YfeB, <i>H. influenzae</i> , e-111	<i>yfeB</i>	296	IM
3G1	YPO3144	MdlB, <i>E. coli</i> , e0.0	<i>MdlB</i>	607	IM
2B3	YPO0337	no simil.	-	141	OM
5G6	YPO1987	putative PP of <i>S. typhimurium</i> , e-146	-	552	?
1D12	YPO1994	no simil.	-	316	?
5A5	YPO3572	Putative EC protein of <i>S. enterica</i> , 2e-91	-	207	PP or OM
4H2	YPO2712	RseA	<i>rseA</i>	218	
1A9	YPO2532	no simil.	-	-	?
5E4	YPO0702	low similarity to various putative secreted proteins of the same size		331	OM or PP
2G5	YPO1485	hyp. protein VCA0110 <i>V. cholerae</i> , 3e-66	-	587	?
3G6	YPO2503	no simil.	-	222	?
2G10	YPO1483	no simil.	-	533	?
1H9	YPO1696	various usher proteins	-	815	OM
4F4	YopH	YopH	<i>yopH</i>	468	EC
4G11	YPO3010	YopM <i>Y. ent.</i>	<i>yopM-2</i>	410	EC

Genes involved in polysaccharide biosynthesis:

One third of the sequenced mutants had transposon insertions in genes related to polysaccharide biosynthesis (mainly LPS core or O-antigen biosynthesis). In five cases (1B3, 1D2, 1D9, 3G2 and 3F3; Table 1) the genes disrupted belong to a single characterized O-antigen biosynthesis locus of *Y. pseudotuberculosis*. The disrupted genes encode mannose-phosphate-guanylyl transferase YPO3099 (1D2), fucose synthetase YPO3100 (3G2), LPS core biosynthesis protein YPO3104 (1B3), sugar dehydratase YPO3114 (1D9) and ascarylose biosynthesis protein YPO3116 (3F3). These genes are also present in *Y. pestis*. Other genes related to polysaccharide biosynthesis, such as those encoding UDP-glucose 6-dehydrogenase (1H10) and glycosyltransferase (4H9) were also identified. One mutant, 3H10, contained an insert in a putative promoter region of a single-gene operon encoding glycosyltransferase. The only mutation in an LPS-related gene which was absent in *Y. pestis* encoded an O-antigen transporter (5D12).

Putative virulence-related genes with orthologues in other bacteria:

Putative interrupted virulence genes include those encoding phospholipase A (*pldA*) (3F10), sensory transducer His kinase VirA (1G6-1), a putative adhesin (2G8), a Pro-dipeptidase (5E6), RseA, a negative regulator of sigma 24 transcription factor (4H2) a transcription activator (5H10) and a transcription regulator (5A5) flanked by a *vspC* gene essential for secretion of virulence factors. The genes found in 4H10 and 3G1 are related to ABC transporters, a large class of proteins involved in export-import of a range of molecules. A clue to their possible function can be found from the analysis of corresponding regions of *Y. pestis*. In the case of 3G1, other genes of the operon are involved in ammonia assimilation. These genes are assumed to be essential *in vivo*, when bacteria have a depleted source of nitrogen. Similarly, the *Y. pestis* orthologue of the gene disrupted in the ABC transporter (4H10) is also located in the region involved in nitrate, as well as amino acid, transport. An unusual feature of this region in *Y. pestis* is that this gene overlaps by 270 nucleotides with another gene (AMP nucleosidase) transcribed in the opposite direction. Disrupted genes in the iron-III dicitrate ATP-binding protein 5G7 is likely to be involved in iron transport.

Unknown and hypothetical genes:

Six mutants (1G6, 5D12, 5H10, 5B12, 1A9-1 and 1C9) contained inserts into genes with unknown function. Two of them (1C9 and 1A9-1) did not have counterparts in *Y. pestis*. Both these mutants contained inserts in the region identical to an *E. coli* integrase-recombinase pseudogene, but actually had inserts into an adjacent region

similar to an *E. coli* gene with unknown function. Transposon integration sites in these mutants were separated by approximately 200 nucleotides. A region flanking the insertion site in the 1G6 appeared to be unique for *Yersinia* as it had 97% identity in the *Y. pestis* database, whereas no similarity to other bacteria was found. Genes in mutants 3C10 and 5B12 have similarities in a non-redundant database (nrdb) and also have counterparts in *Y. pestis*. The genes inactivated in mutants 2B3, 5G6, 1D12 and 1A9 appear to be unique for *Yersinia*, as no homologues could be identified in a nrdb. Genes inactivated in certain mutants do not have *Y. pestis* orthologues. One of these mutants (5D12) contains insert in the gene encoding a putative O-antigen transferase (see above).

In vivo and *in vitro* competition studies:

For *in vivo* competition studies, mutant and wild-type strains were grown separately to exponential phase in LB media with appropriate antibiotics. Bacteria were washed with LB media and the concentration adjusted to 5×10^6 cfu/ml. Equal volumes of each bacterial suspension were mixed together and 0.1 ml volumes were injected iv into 4 mice as above. Viable counts on LB, LB-Nal and LB-Nal-Kan allowed the exact input ratio to be calculated. After 3 days, spleens were recovered and passed through sieves (70 μ m, Becton Dickinson) to produce a cell suspension in 3 ml LB. Homogenates were plated on selective media to determine the output ratio. The competitive index is defined as the output ratio (mutant/wt) divided by the input ratio (mutant/wt).

In-vitro CI was determined as described in Chiang *et al.*, Mol. Microbiol., 1998; 27: 797-805. Briefly, mixtures containing a mutant and the wild-type strains were inoculated into LB media supplemented with nalidixic acid at approximately 1×10^4 cfu/ml. The cultures were grown overnight at 28°C and the mutant to wild-type ratios were determined by plating on media with and without selective marker (kanamycin).

The majority of the selected mutants with reduced output signals did not reveal significant reduction in *in vitro* growth properties and were confirmed to be attenuated (Table 1). Four mutants (1D9, 1D2, 4H9 and 3H10) revealed substantial (more than six times) reduction in CI. In all cases, the genes affected are related to LPS or LPS core biosynthesis. For example, an orthologue to a gene inactivated in 4H10 is located in an operon containing a number of other genes, such as *kdtB*, *waaA*, *rfaC*, *rfaD* and *rfaF*, all related to core biosyntheses. The insert in mutant 3H10 would also inactivate a gene encoding an LPS core-related glycosyltransferase. Inactivation of genes in other

mutants of this class may have a dramatic effect on outer membrane stability due to an affect on LPS biosynthesis.

In vivo CI figures of less than 0.3 were demonstrated in 14 out of 20 cases, confirming attenuated properties of these mutants.

In vivo competition studies revealed significant attenuation of the 3F10 (PldA) derivative. The competitive index (CI=0.01655) obtained in the mixed infection experiment confirmed that the strain was severely attenuated. These data suggest that *PldA* is an essential virulence factor in the murine yersiniosis model of infection.

CLAIMS

1. A peptide encoded by a gene comprising any of the nucleotide sequences identified herein as SEQ ID NOS. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 57, 58 and 64, of *Yersinia pseudotuberculosis*, or a related molecule having at least 60% sequence similarity or identity at the peptide level in a Gram-negative bacterium, or a functional fragment thereof, for therapeutic or diagnostic use.
2. A peptide according to claim 1, wherein the sequence similarity or identity is at least 80%.
3. A peptide according to claim 1 or claim 2, wherein the sequence similarity or identity is at least 90%.
4. A peptide according to claim 1, comprising any of the amino acid sequences identified herein as SEQ ID NO. 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55 and 65.
5. A polynucleotide encoding a peptide according to any preceding claim, for therapeutic or diagnostic use.
6. A recombinant host genetically modified to express a peptide according to any of claims 1 to 4.
7. An attenuated microorganism comprising a mutation that disrupts the expression of the nucleotide sequence defined in claim 1 or that identified herein as SEQ ID NO. 59, 60, 61, 62 or 63, or homologue thereof.
8. A microorganism according to claim 7, wherein the mutation is insertional inactivation or a gene deletion.
9. A microorganism according to claim 7 or claim 8, wherein the microorganism is *Yersinia pseudotuberculosis* or *Yersinia pestis*.
10. A microorganism according to any of claims 7 to 9, comprising a second mutation in a second nucleotide sequence.
11. A microorganism according to any of claims 7 to 10, comprising a heterologous antigen, therapeutic peptide or nucleic acid.
12. A microorganism according to any of claims 7 to 11, for therapeutic or diagnostic use.
13. A vaccine comprising a peptide according to any of claims 1 to 4.
14. A vaccine comprising a microorganism according to any of claims 7 to 12.
15. An antibody raised against a peptide according to any of claims 1 to 4.

16. Use of a product according to any of claims 1 to 12, for the manufacture of a medicament for use in the treatment or prevention of a condition associated with infection by *Yersinia*.

17. Use according to claim 16, wherein the condition is tuberculosis.

18. Use according to claim 16 or claim 17, for veterinary treatment.

19. Use of a peptide, polynucleotide or microorganism, according to any of claims 1 to 12, in a screening assay for the identification of an antimicrobial drug.

SEQUENCE LISTING

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<120> Virulence Genes, Proteins, and Their Use

<130> REP06947WO

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Tyr Pro Asp Arg Val Thr Arg Leu Tyr Pro His His Gln Tyr Arg Tyr
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aac gat aat tta gtc cat gaa tca ctc gat agc ggc tca gca aaa gtt 480
Asn Asp Asn Leu Val His Glu Ser Leu Asp Ser Gly Ser Ala Lys Val
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Arg His Gln Gln Gly Lys Ser Cys Ser Tyr Phe Ala Ile Leu Ser His
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Thr Leu Gly Ala Phe Ser Lys Thr Trp Leu Leu Arg Ala Gly Phe Leu
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Gln Gln Phe Gly Ala Lys Val Tyr Ser Asn Ile Asn Trp Pro Gly Tyr
 50 55 60

Gly Lys Gln Arg Gln Leu Ala Gln Gln Tyr Ala Ser Gly Asp Tyr Ile
 65 70 75 80

Leu Met Leu Asp Ala Asp Glu Arg Val Thr Pro Glu Leu Lys Ile Ala
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Ile Glu Ser Val Leu Leu Ala Pro Glu Glu Gly Ala Val Tyr Ser Cys
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Ser Arg Arg Asn Leu Phe Leu Gly Arg Phe Met Arg His Ser Gly Trp
 115 120 125

Tyr Pro Asp Arg Val Thr Arg Leu Tyr Pro His His Gln Tyr Arg Tyr
 130 135 140

Asn Asp Asn Leu Val His Glu Ser Leu Asp Ser Gly Ser Ala Lys Val
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Ile Pro Leu Ala Gly Asp Leu Leu His Leu Thr Cys Arg Asp Phe Phe
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 180 185 190

Arg His Gln Gln Gly Lys Ser Cys Ser Tyr Phe Ala Ile Leu Ser His
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Thr Leu Gly Ala Phe Ser Lys Thr Trp Leu Leu Arg Ala Gly Phe Leu
 210 215 220

Asp Gly Lys Gln Gly Leu Leu Leu Ala Val Val Asn Ala Gln Tyr Thr
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ggc atg att ata aat aaa ttt cat tca ggc cag gtt gat ggg aaa cct 144
 Gly Met Ile Ile Asn Lys Phe His Ser Gly Gln Val Asp Gly Lys Pro
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tat ttc tgc att gag gca ttc aag ccg tca aca acg ata aca gcc tgt 192
 Tyr Phe Cys Ile Glu Ala Phe Lys Pro Ser Thr Thr Ile Thr Ala Cys
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 Ser Val Lys Asp Thr Ser Ile Trp Gly Ala Ser Tyr Asn Thr Leu Tyr
 65 70 75 80

gat cag gct atg tat tat tat aca acc ggt aag cgt atc aga gtt tat 288
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 85 90 95

tac gct ccg gat gtc tgg act aat aat agt ttt gtg agg gca ctt aca 336
 Tyr Ala Pro Asp Val Trp Thr Asn Asn Ser Phe Val Arg Ala Leu Thr

100 105 110
gca aat gct ctg gtt gga ttc tca acg tgt atc tcg gaa agt tcg tgc 384
Ala Asn Ala Leu Val Gly Phe Ser Thr Cys Ile Ser Glu Ser Ser Cys
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Tyr Phe Cys Ile Glu Ala Phe Lys Pro Ser Thr Thr Ile Thr Ala Cys
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Ser Val Lys Asp Thr Ser Ile Trp Gly Ala Ser Tyr Asn Thr Leu Tyr
65 70 75 80

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Tyr Ala Pro Asp Val Trp Thr Asn Asn Ser Phe Val Arg Ala Leu Thr
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gtc gag tat aca gtc tgc agc aat gag gat tta cac tgg ctg gat caa 144
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cgt atc tcc atg ccg aaa gat gtt ttc atc gac ggg caa tat gtg cgt 624
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 35 40 45

acc gca tcc tgc gaa tca aaa atc acc tat att gat ggt gat cag ggt 192
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 65 70 75 80

Thr Tyr Leu Glu Val Cys Tyr Ile Leu Leu Tyr Gly Glu Thr Pro Thr
 85 90 95

Pro Glu Glu Tyr Lys Thr Phe Lys Thr Thr Val Thr Arg His Thr Met
 100 105 110

Ile His Glu Gln Ile Thr Arg Leu Phe His Gly Phe Arg Arg Asp Ser
 115 120 125

His Pro Met Ala Val Leu Cys Gly Val Thr Gly Ala Leu Ala Ala Phe
 130 135 140

Tyr His Asp Ala Leu Asp Val Asn Asn Glu Arg His Arg Glu Ile Thr
 145 150 155 160

Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Val Ala Ala Met Cys Tyr
 165 170 175

Lys Tyr Ser Leu Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu Ser
 180 185 190

Tyr Ala Gly Asn Phe Leu His Met Met Phe Ser Thr Pro Cys Glu Lys
 195 200 205

Tyr Glu Val Asn Pro Val Leu Glu Arg Ala Met Asp Arg Ile Leu Ile
 210 215 220

Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg Thr
 225 230 235 240

Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly Ile
 245 250 255

Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Cys Leu
 260 265 270
 Lys Met Leu Glu Glu Ile Lys Thr Val Glu His Ile Pro Glu Phe Ile
 275 280 285
 Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe Gly
 290 295 300
 His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg Glu
 305 310 315 320
 Thr Cys His Glu Val Leu Glu Glu Leu Lys Leu Asn Asn Ser Leu Leu
 325 330 335
 Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr Phe
 340 345 350
 Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile Ile
 355 360 365
 Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe Ala
 370 375 380
 Ile Ala Arg Thr Ile Gly Trp Ile Ala His Trp Asn Glu Met His Asn
 385 390 395 400
 Asp Gly Ile Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr Thr
 405 410 415
 Glu Arg Asp Phe Gln Ser Gln Leu Lys Lys
 420 425

<210> 9

<211> 930

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(930)

<400> 9

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1	5	10	15	
ttt aac aac tca aat tca att caa aaa tat act gga gca gtc tca tct				96
Phe Asn Asn Ser Asn Ser Ile Gln Lys Tyr Thr Gly Ala Val Ser Ser				
	20	25	30	
ata agt gat gat tta cgt att aat aat gaa aag tgc aag agt gac ata				144
Ile Ser Asp Asp Leu Arg Ile Asn Asn Glu Lys Cys Lys Ser Asp Ile				
	35	40	45	
gga act ata agt ggt gat ata aaa att aat cgc cat tct gca gtc tac				192
Gly Thr Ile Ser Gly Asp Ile Lys Ile Asn Arg His Ser Ala Val Tyr				
	50	55	60	
ggt aat gtg aat tca gtc agt ggc gat att act gta aaa aat tct ata				240
Gly Asn Val Asn Ser Val Ser Gly Asp Ile Thr Val Lys Asn Ser Ile				
	65	70	75	80
gta gat aaa gac atc acc aca gta agt ggt gat gtt aac gcg gtg aat				288
Val Asp Lys Asp Ile Thr Thr Val Ser Gly Asp Val Asn Ala Val Asn				
	85	90	95	
tcg act ata gga aaa aat ata aaa aca gtc agt ggt tcg att gag gtg				336
Ser Thr Ile Gly Lys Asn Ile Lys Thr Val Ser Gly Ser Ile Glu Val				
	100	105	110	
gaa caa tca act gta agc ggc aat ttg gaa aca aca agt ggt ggg ata				384
Glu Gln Ser Thr Val Ser Gly Asn Leu Glu Thr Thr Ser Gly Gly Ile				
	115	120	125	
gat ata gat aca aca aaa att aac ggt aat gtg cat acg aca agt ggt				432
Asp Ile Asp Thr Thr Lys Ile Asn Gly Asn Val His Thr Thr Ser Gly				
	130	135	140	
tca att tcg atg aac gat tca act att gat ggt agc gta aca tgt aag				480
Ser Ile Ser Met Asn Asp Ser Thr Ile Asp Gly Ser Val Thr Cys Lys				
	145	150	155	160
gcg ggg tct gta aca att gtc aat tca aca att aaa gaa agc ctt aat				528
Ala Gly Ser Val Thr Ile Val Asn Ser Thr Ile Lys Glu Ser Leu Asn				
	165	170	175	
gta acc agt gag aaa ata att gtt ggt aca gca tct tgt att gga aaa				576
Val Thr Ser Glu Lys Ile Ile Val Gly Thr Ala Ser Cys Ile Gly Lys				
	180	185	190	
att aac att tcc ccc cct gaa tct gta aat ttt aac atc atg aat ttt				624
Ile Asn Ile Ser Pro Pro Glu Ser Val Asn Phe Asn Ile Met Asn Phe				

195	200	205	
ggg aac gat agt ata gtg atg gga atg agg aat ttt tgt att tca gga			672
Gly Asn Asp Ser Ile Val Met Gly Met Arg Asn Phe Cys Ile Ser Gly			
210	215	220	
gag gta aat ttt acc att act aat ggt aaa gta ttt gtt aat gaa caa			720
Glu Val Asn Phe Thr Ile Thr Asn Gly Lys Val Phe Val Asn Glu Gln			
225	230	235	240
agg gtc ggc cat aca gct tcg caa tca act tcg aaa aaa gta gaa gaa			768
Arg Val Gly His Thr Ala Ser Gln Ser Thr Ser Lys Lys Val Glu Glu			
245	250	255	
gtt act att aat atc gcg aaa aat gcc agt gtt aat gat att gtt ttt			816
Val Thr Ile Asn Ile Ala Lys Asn Ala Ser Val Asn Asp Ile Val Phe			
260	265	270	
tat act aaa aag tgc cat atc att tta gaa gga aat gct aaa tat aac			864
Tyr Thr Lys Lys Cys His Ile Ile Leu Glu Gly Asn Ala Lys Tyr Asn			
275	280	285	
gga gaa aaa aag gat ggc atg caa ttc acc cat gtt aac gca ccg aaa			912
Gly Glu Lys Lys Asp Gly Met Gln Phe Thr His Val Asn Ala Pro Lys			
290	295	300	
agt cat gct tat gcg taa			930
Ser His Ala Tyr Ala			
305	310		
<210> 10			
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<212> PRT			
<213> Yersinia pestis			
<400> 10			
Met Pro Gln Val Asn Asn Ile Ser Thr Asn Asn Ile His Ser Ala Gly			
1	5	10	15
Phe Asn Asn Ser Asn Ser Ile Gln Lys Tyr Thr Gly Ala Val Ser Ser			
20	25	30	
Ile Ser Asp Asp Leu Arg Ile Asn Asn Glu Lys Cys Lys Ser Asp Ile			
35	40	45	
Gly Thr Ile Ser Gly Asp Ile Lys Ile Asn Arg His Ser Ala Val Tyr			
50	55	60	

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 <212> DNA
 <213> *Yersinia pestis*

<220>
 <221> CDS
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 1 5 10 15
 aac gat acc aaa ata gca gaa atc att aag ctg gct gat ttt gaa gtg 96
 Asn Asp Thr Lys Ile Ala Glu Ile Ile Lys Leu Ala Asp Phe Glu Val
 20 25 30
 aac aac gca gat gtc gtt aat ttt ctt aaa aaa gaa gac gaa gcc ggt 144
 Asn Asn Ala Asp Val Val Asn Phe Leu Lys Lys Glu Asp Glu Ala Gly
 35 40 45
 tat cag gat tgc cct gat ctg gtg atg gcg cat ttt ctg aat ggt ttg 192
 Tyr Gln Asp Cys Pro Asp Leu Val Met Ala His Phe Leu Asn Gly Leu
 50 55 60
 att ttc ttt aga cgt ggt aaa gat gat aag ttc cct gca cct gcg gta 240
 Ile Phe Phe Arg Arg Gly Lys Asp Asp Lys Phe Pro Ala Pro Ala Val
 65 70 75 80
 gag gcg gtt atc acc aac aat att gtg ttg aaa aaa ctg cgt gtc gca 288
 Glu Ala Val Ile Thr Asn Asn Ile Val Leu Lys Lys Leu Arg Val Ala
 85 90 95
 ttc gaa ttg aaa gac acc gat atg cat gat gtt ttt aat gcc gtt gaa 336
 Phe Glu Leu Lys Asp Thr Asp Met His Asp Val Phe Asn Ala Val Glu
 100 105 110
 ttc cca gtc tct aag cct gag tta aat gct ctg ttc cgt aaa gag ggc 384
 Phe Pro Val Ser Lys Pro Glu Leu Asn Ala Leu Phe Arg Lys Glu Gly
 115 120 125
 agc aaa aac ttc cgc cct tgt ggt gat cag gtt tta cgt tat ttt ctg 432
 Ser Lys Asn Phe Arg Pro Cys Gly Asp Gln Val Leu Arg Tyr Phe Leu
 130 135 140

aag ggc ctg aca ctg cgt att cgt ggc gct aaa aaa gcc tag 474
 Lys Gly Leu Thr Leu Arg Ile Arg Gly Ala Lys Lys Ala
 145 150 155

<210> 12

<211> 157

<212> PRT

<213> Yersinia pestis

<400> 12

Met Ile Asn Asn Asp Val Leu Arg Ser Val Arg Tyr Met Leu Asn Val
 1 5 10 15

Asn Asp Thr Lys Ile Ala Glu Ile Ile Lys Leu Ala Asp Phe Glu Val
 20 25 30

Asn Asn Ala Asp Val Val Asn Phe Leu Lys Lys Glu Asp Glu Ala Gly
 35 40 45

Tyr Gln Asp Cys Pro Asp Leu Val Met Ala His Phe Leu Asn Gly Leu
 50 55 60

Ile Phe Phe Arg Arg Gly Lys Asp Asp Lys Phe Pro Ala Pro Ala Val
 65 70 75 80

Glu Ala Val Ile Thr Asn Asn Ile Val Leu Lys Lys Leu Arg Val Ala
 85 90 95

Phe Glu Leu Lys Asp Thr Asp Met His Asp Val Phe Asn Ala Val Glu
 100 105 110

Phe Pro Val Ser Lys Pro Glu Leu Asn Ala Leu Phe Arg Lys Glu Gly
 115 120 125

Ser Lys Asn Phe Arg Pro Cys Gly Asp Gln Val Leu Arg Tyr Phe Leu
 130 135 140

Lys Gly Leu Thr Leu Arg Ile Arg Gly Ala Lys Lys Ala
 145 150 155

<210> 13

<211> 675

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(675)

<400> 13

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Met Asn Glu Asn Trp Asn Trp Ser Leu Val Asp Lys Val Val Tyr Ile
  1             5             10             15

aat ttg aag gaa cgt acg gat aga aat gag cac atc aaa aaa gaa ctg 96
Asn Leu Lys Glu Arg Thr Asp Arg Asn Glu His Ile Lys Lys Glu Leu
      20             25             30

gaa aaa gtg tgc ttt cca cct gaa aaa ata atc cgc ttt gag gca ata 144
Glu Lys Val Cys Phe Pro Pro Glu Lys Ile Ile Arg Phe Glu Ala Ile
      35             40             45

aga gca ggg tca ggt ttt atc ggt tgc gca aaa tca cat ctt gca gta 192
Arg Ala Gly Ser Gly Phe Ile Gly Cys Ala Lys Ser His Leu Ala Val
      50             55             60

tta aaa atg gcg caa gag aat aat tgg aga aat att ttg ata ctt gaa 240
Leu Lys Met Ala Gln Glu Asn Asn Trp Arg Asn Ile Leu Ile Leu Glu
      65             70             75             80

gac gat atg gtc ttc gaa gat gat gat gaa aca att atc cgg aca aac 288
Asp Asp Met Val Phe Glu Asp Asp Asp Glu Thr Ile Ile Arg Thr Asn
      85             90             95

aat ttt ctc tct aaa ctg aat aat att cat tgg gat gct gca ttt tta 336
Asn Phe Leu Ser Lys Leu Asn Asn Ile His Trp Asp Ala Ala Phe Leu
      100             105             110

tcc gcc agc tat tat atc gtt aac gct att gat gat aat ttt ttt aaa 384
Ser Ala Ser Tyr Tyr Ile Val Asn Ala Ile Asp Asp Asn Phe Phe Lys
      115             120             125

gtc aat ttc gcc tat ctg gct aac agc tat ctg gtc aat aat cat tat 432
Val Asn Phe Ala Tyr Leu Ala Asn Ser Tyr Leu Val Asn Asn His Tyr
      130             135             140

tat gaa aaa tta atc aat aac tac acg gag tct gtt cag cga tta aca 480
Tyr Glu Lys Leu Ile Asn Asn Tyr Thr Glu Ser Val Gln Arg Leu Thr
      145             150             155             160

aat ggc gag tca tcg tca gag tac ggg ttg gat tct aac tgg ttg aaa 528
Asn Gly Glu Ser Ser Ser Glu Tyr Gly Leu Asp Ser Asn Trp Leu Lys

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165 170 175
 ata atg aaa ata gac aac tgg tac gga att tac ccg gtt att ggc tat 576
 Ile Met Lys Ile Asp Asn Trp Tyr Gly Ile Tyr Pro Val Ile Gly Tyr
 180 185 190

 cag cgt acc gat atc agt gat att gaa tat aaa gag atc gat cgc aca 624
 Gln Arg Thr Asp Ile Ser Asp Ile Glu Tyr Lys Glu Ile Asp Arg Thr
 195 200 205

 cac cag ttc acc cga aca ttc gat aag atg aaa gca tac ggt tca aaa 672
 His Gln Phe Thr Arg Thr Phe Asp Lys Met Lys Ala Tyr Gly Ser Lys
 210 215 220

 taa 675

225

<210> 14

<211> 224

<212> PRT

<213> Yersinia pestis

<400> 14

Met Asn Glu Asn Trp Asn Trp Ser Leu Val Asp Lys Val Val Tyr Ile
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Asn Leu Lys Glu Arg Thr Asp Arg Asn Glu His Ile Lys Lys Glu Leu
 20 25 30

Glu Lys Val Cys Phe Pro Pro Glu Lys Ile Ile Arg Phe Glu Ala Ile
 35 40 45

Arg Ala Gly Ser Gly Phe Ile Gly Cys Ala Lys Ser His Leu Ala Val
 50 55 60

Leu Lys Met Ala Gln Glu Asn Asn Trp Arg Asn Ile Leu Ile Leu Glu
 65 70 75 80

Asp Asp Met Val Phe Glu Asp Asp Asp Glu Thr Ile Ile Arg Thr Asn
 85 90 95

Asn Phe Leu Ser Lys Leu Asn Asn Ile His Trp Asp Ala Ala Phe Leu
 100 105 110

Ser Ala Ser Tyr Tyr Ile Val Asn Ala Ile Asp Asp Asn Phe Phe Lys
 115 120 125

Val Asn Phe Ala Tyr Leu Ala Asn Ser Tyr Leu Val Asn Asn His Tyr
 130 135 140

Tyr Glu Lys Leu Ile Asn Asn Tyr Thr Glu Ser Val Gln Arg Leu Thr
 145 150 155 160

Asn Gly Glu Ser Ser Ser Glu Tyr Gly Leu Asp Ser Asn Trp Leu Lys
 165 170 175

Ile Met Lys Ile Asp Asn Trp Tyr Gly Ile Tyr Pro Val Ile Gly Tyr
 180 185 190

Gln Arg Thr Asp Ile Ser Asp Ile Glu Tyr Lys Glu Ile Asp Arg Thr
 195 200 205

His Gln Phe Thr Arg Thr Phe Asp Lys Met Lys Ala Tyr Gly Ser Lys
 210 215 220

<210> 15

<211> 1659

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(1659)

<400> 15

ttg agc ttc gct cat gca cag aca ttg ccc gat gtc tat tca gtg gtt 48
 Leu Ser Phe Ala His Ala Gln Thr Leu Pro Asp Val Tyr Ser Val Val
 1 5 10 15

gaa cga aaa ctg gaa aat gcc cta ccg ctg gcg gaa cac ccc cat tat 96
 Glu Arg Lys Leu Glu Asn Ala Leu Pro Leu Ala Glu His Pro His Tyr
 20 25 30

gat gct cag gcc cct tat ttc gaa ctg cac cga gaa atc ctg atg ttt 144
 Asp Ala Gln Ala Pro Tyr Phe Glu Leu His Arg Glu Ile Leu Met Phe
 35 40 45

agc tca cca gaa cga gcc aat acg cta tta aag aaa ctt gat ttc agt 192
 Ser Ser Pro Glu Arg Ala Asn Thr Leu Leu Lys Lys Leu Asp Phe Ser
 50 55 60

tcg aaa gag gca atg tta tca ctg aat att tct gct gac tgg att gcg 240

22

Ser Gly Ile Met Ala Phe Tyr His Ala Asn Gly Phe Thr Glu Glu Tyr
 260 265 270

aat gca tta att gca acc agc att gcc act aca gat aag tcc ttt agc 864
 Asn Ala Leu Ile Ala Thr Ser Ile Ala Thr Thr Asp Lys Ser Phe Ser
 275 280 285

ttt gct ccc aag cct ata gaa gaa ata aag ctt atc cgg ttg ttg aat 912
 Phe Ala Pro Lys Pro Ile Glu Glu Ile Lys Leu Ile Arg Leu Leu Asn
 290 295 300

gcc act aac gaa acc ggc cta att aaa gag cgt att gat aag ctg atg 960
 Ala Thr Asn Glu Thr Gly Leu Ile Lys Glu Arg Ile Asp Lys Leu Met
 305 310 315 320

atc tca cca gaa tat gcc tgt tat gac gat aga tat tgc tat gaa tat 1008
 Ile Ser Pro Glu Tyr Ala Cys Tyr Asp Asp Arg Tyr Cys Tyr Glu Tyr
 325 330 335

aaa ata gat tcg ctt aat ttt cta tat tta agc aaa tct gat gca tta 1056
 Lys Ile Asp Ser Leu Asn Phe Leu Tyr Leu Ser Lys Ser Asp Ala Leu
 340 345 350

gct gat aaa tat tta aac att att att gaa gaa tca caa aat caa aaa 1104
 Ala Asp Lys Tyr Leu Asn Ile Ile Ile Glu Glu Ser Gln Asn Gln Lys
 355 360 365

ttc aat cca tgg gaa acg gta act aaa tcc atc gtt aaa aaa tta gtt 1152
 Phe Asn Pro Trp Glu Thr Val Thr Lys Ser Ile Val Lys Lys Leu Val
 370 375 380

gat att gga cgt atc gcc gaa gct aag aag ttg gct gca gat gca gag 1200
 Asp Ile Gly Arg Ile Ala Glu Ala Lys Lys Leu Ala Ala Asp Ala Glu
 385 390 395 400

gtt att tat ctc tca cag cta aaa gac tct ccg ccc aaa gaa gtc gaa 1248
 Val Ile Tyr Leu Ser Gln Leu Lys Asp Ser Pro Pro Lys Glu Val Glu
 405 410 415

aga aat tat agg gat ctt gct gaa atg tat ggt ttt gca ggc gat gtc 1296
 Arg Asn Tyr Arg Asp Leu Ala Glu Met Tyr Gly Phe Ala Gly Asp Val
 420 425 430

gtc agc gct gaa cga ata ctt aat aag cat gtc acc acc gcc caa aat 1344
 Val Ser Ala Glu Arg Ile Leu Asn Lys His Val Thr Thr Ala Gln Asn
 435 440 445

tac ttt att acc gat ctg ttt ata aaa aat aaa cag tgg gat gaa gcc 1392

Tyr Phe Ile Thr Asp Leu Phe Ile Lys Asn Lys Gln Trp Asp Glu Ala
 450 455 460
 aga gcg cgt gtt gtg aaa gat acc ggt ctt tct gga caa aac ctg acg 1440
 Arg Ala Arg Val Val Lys Asp Thr Gly Leu Ser Gly Gln Asn Leu Thr
 465 470 475 480
 tta ttg caa aat att tgt gct acc aat aca cct gaa tgc atg caa cat 1488
 Leu Leu Gln Asn Ile Cys Ala Thr Asn Thr Pro Glu Cys Met Gln His
 485 490 495
 atc acg ttc aca ctt aaa tca atg tta aca cgt gaa tcc att acc gca 1536
 Ile Thr Phe Thr Leu Lys Ser Met Leu Thr Arg Glu Ser Ile Thr Ala
 500 505 510
 gaa gat gca tca ggg aat caa caa ctc tac cag ttg ggg atc atc tac 1584
 Glu Asp Ala Ser Gly Asn Gln Gln Leu Tyr Gln Leu Gly Ile Ile Tyr
 515 520 525
 cac tct ctt ggg ata aag ccg acc gag gaa caa cag ctt ctc att caa 1632
 His Ser Leu Gly Ile Lys Pro Thr Glu Glu Gln Gln Leu Leu Ile Gln
 530 535 540
 aaa tta tat gat aat gcg gcg gcc taa 1659
 Lys Leu Tyr Asp Asn Ala Ala Ala
 545 550

<210> 16

<211> 552

<212> PRT

<213> Yersinia pestis

<400> 16

Leu Ser Phe Ala His Ala Gln Thr Leu Pro Asp Val Tyr Ser Val Val
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 20 25 30
 Asp Ala Gln Ala Pro Tyr Phe Glu Leu His Arg Glu Ile Leu Met Phe
 35 40 45
 Ser Ser Pro Glu Arg Ala Asn Thr Leu Leu Lys Lys Leu Asp Phe Ser
 50 55 60
 Ser Lys Glu Ala Met Leu Ser Leu Asn Ile Ser Ala Asp Trp Ile Ala
 65 70 75 80

Gly Thr Gly Asn Pro Asp Lys Ala Met Val Phe Leu Ser Gln Ile Gly
 85 90 95
 Leu Glu Lys Pro Ser Ser Phe Ser Ala Tyr Lys Asn Tyr Val Asp Ala
 100 105 110
 Trp Ile Glu Lys Lys Gln Pro Glu Ser Ala Leu Lys Leu Leu Met Leu
 115 120 125
 Asp Asn Ser Ala Arg Asn Tyr Tyr Leu Pro Ala Val Leu Asp Ala Tyr
 130 135 140
 Arg Asp Thr Pro Asp Gln Ala Val Thr Ile Tyr Lys Asp Ile Tyr Gly
 145 150 155 160
 Asp Asn Ile Ile Glu Pro Thr Asn Gln Leu Arg Met Leu Leu Ala Ile
 165 170 175
 Ala Glu Asn Tyr Arg Val Asn Gly Ala Pro Lys Asn Thr Leu Ile Tyr
 180 185 190
 Thr Asp Lys Ala Gln Val Met Phe Ile Asp Val Leu Lys Lys Lys Lys
 195 200 205
 Asn Asn Glu Ile His Phe Tyr Lys Asp Tyr Leu Asn Leu Ile Asn Leu
 210 215 220
 Tyr Ser Phe Ala Gly Asn Lys Gln Gln Ala Leu Ile Leu Ser Glu Gln
 225 230 235 240
 Leu Leu Arg Ala Ala Gly Asp Lys Gly Thr Tyr Tyr Asp Leu Ala Leu
 245 250 255
 Ser Gly Ile Met Ala Phe Tyr His Ala Asn Gly Phe Thr Glu Glu Tyr
 260 265 270
 Asn Ala Leu Ile Ala Thr Ser Ile Ala Thr Thr Asp Lys Ser Phe Ser
 275 280 285
 Phe Ala Pro Lys Pro Ile Glu Glu Ile Lys Leu Ile Arg Leu Leu Asn
 290 295 300
 Ala Thr Asn Glu Thr Gly Leu Ile Lys Glu Arg Ile Asp Lys Leu Met
 305 310 315 320
 Ile Ser Pro Glu Tyr Ala Cys Tyr Asp Asp Arg Tyr Cys Tyr Glu Tyr
 325 330 335

Lys Ile Asp Ser Leu Asn Phe Leu Tyr Leu Ser Lys Ser Asp Ala Leu
 340 345 350

Ala Asp Lys Tyr Leu Asn Ile Ile Ile Glu Glu Ser Gln Asn Gln Lys
 355 360 365

Phe Asn Pro Trp Glu Thr Val Thr Lys Ser Ile Val Lys Lys Leu Val
 370 375 380

Asp Ile Gly Arg Ile Ala Glu Ala Lys Lys Leu Ala Ala Asp Ala Glu
 385 390 395 400

Val Ile Tyr Leu Ser Gln Leu Lys Asp Ser Pro Pro Lys Glu Val Glu
 405 410 415

Arg Asn Tyr Arg Asp Leu Ala Glu Met Tyr Gly Phe Ala Gly Asp Val
 420 425 430

Val Ser Ala Glu Arg Ile Leu Asn Lys His Val Thr Thr Ala Gln Asn
 435 440 445

Tyr Phe Ile Thr Asp Leu Phe Ile Lys Asn Lys Gln Trp Asp Glu Ala
 450 455 460

Arg Ala Arg Val Val Lys Asp Thr Gly Leu Ser Gly Gln Asn Leu Thr
 465 470 475 480

Leu Leu Gln Asn Ile Cys Ala Thr Asn Thr Pro Glu Cys Met Gln His
 485 490 495

Ile Thr Phe Thr Leu Lys Ser Met Leu Thr Arg Glu Ser Ile Thr Ala
 500 505 510

Glu Asp Ala Ser Gly Asn Gln Gln Leu Tyr Gln Leu Gly Ile Ile Tyr
 515 520 525

His Ser Leu Gly Ile Lys Pro Thr Glu Glu Gln Gln Leu Leu Ile Gln
 530 535 540

Lys Leu Tyr Asp Asn Ala Ala Ala
 545 550

<210> 17

<211> 951

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1)...(951)

<400> 17

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  1             5             10             15

gat tta tta gga att ttg agt cac tca tcg gca att tcc aat gtg gca 96
Asp Leu Leu Gly Ile Leu Ser His Ser Ser Ala Ile Ser Asn Val Ala
      20             25             30

aat ggg att tat gtg gaa agc gaa atc ctt gaa gta ggt tca tgg ctt 144
Asn Gly Ile Tyr Val Glu Ser Glu Ile Leu Glu Val Gly Ser Trp Leu
      35             40             45

tca gcc tac gcg gct aat aaa gat gaa att ttt tcg cag atc att acc 192
Ser Ala Tyr Ala Ala Asn Lys Asp Glu Ile Phe Ser Gln Ile Ile Thr
      50             55             60

gag ttg gag aac cct tat caa ttc cag ctg gag aat gac ata cag gca 240
Glu Leu Glu Asn Pro Tyr Gln Phe Gln Leu Glu Asn Asp Ile Gln Ala
      65             70             75             80

ccg agt ttt att ctt tac agt aat gaa cgc ata act att cgt ctt gtt 288
Pro Ser Phe Ile Leu Tyr Ser Asn Glu Arg Ile Thr Ile Arg Leu Val
      85             90             95

atg tgg ctc cca ttg cag gga aaa tta gat cgg aca cct tat tcc tac 336
Met Trp Leu Pro Leu Gln Gly Lys Leu Asp Arg Thr Pro Tyr Ser Tyr
      100             105             110

gaa gaa gca cat gat cat aat ttt gac ttt tgg aca gtg aat ttt ttt 384
Glu Glu Ala His Asp His Asn Phe Asp Phe Trp Thr Val Asn Phe Phe
      115             120             125

gga ggt ggc tat cga act cgg ctc tat gac tat gat tac gat aaa gtt 432
Gly Gly Gly Tyr Arg Thr Arg Leu Tyr Asp Tyr Asp Tyr Asp Lys Val
      130             135             140

agt ggc gta aat aac gaa gtt gta gaa ctt aat tgt tat gga gat aag 480
Ser Gly Val Asn Asn Glu Val Val Glu Leu Asn Cys Tyr Gly Asp Lys
      145             150             155             160

att ctt tcc ccg aat aca gtt atg ttt tat ttt cgt agt aag gat gtt 528

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Ile Leu Ser Pro Asn Thr Val Met Phe Tyr Phe Arg Ser Lys Asp Val
165 170 175

cat act caa tat ccg cct gat gaa tta tca gta tcg ctc aat tta ata 576
His Thr Gln Tyr Pro Pro Asp Glu Leu Ser Val Ser Leu Asn Leu Ile
180 185 190

gtg cga cca ata aaa tcg aag cat caa tac gaa ttt cag ata gat tca 624
Val Arg Pro Ile Lys Ser Lys His Gln Tyr Glu Phe Gln Ile Asp Ser
195 200 205

gat gca ttg gaa gga aaa ata gag gca aga att aaa aag gga aga tat 672
Asp Ala Leu Glu Gly Lys Ile Glu Ala Arg Ile Lys Lys Gly Arg Tyr
210 215 220

gag cgc tac gct ttt caa aat gtg tta tat aac ggc ctg ctg agt ctt 720
Glu Arg Tyr Ala Phe Gln Asn Val Leu Tyr Asn Gly Leu Leu Ser Leu
225 230 235 240

gaa aat gaa aaa agt cgt caa ctg gtt cac aaa gtg tct ctt tgt aac 768
Glu Asn Glu Lys Ser Arg Gln Leu Val His Lys Val Ser Leu Cys Asn
245 250 255

cat cga gaa gag ata cga tta atc gct tat gaa gct tta ctt aag cac 816
His Arg Glu Glu Ile Arg Leu Ile Ala Tyr Glu Ala Leu Leu Lys His
260 265 270

gcc caa aaa aaa ggt aat gtg agt gat ata aag agc att agt gaa caa 864
Ala Gln Lys Lys Gly Asn Val Ser Asp Ile Lys Ser Ile Ser Glu Gln
275 280 285

gca ttt aaa gac caa agc ctc tat atc aaa aat aag att tct cac agt 912
Ala Phe Lys Asp Gln Ser Leu Tyr Ile Lys Asn Lys Ile Ser His Ser
290 295 300

att gga agc atg cca tgc atg agt cca aaa ccc cgc taa 951
Ile Gly Ser Met Pro Cys Met Ser Pro Lys Pro Arg
305 310 315

<210> 18

<211> 316

<212> PRT

<213> Yersinia pestis

<400> 18

Met Leu Leu Asn Asn Ile Thr Pro Val Asn Lys Ser Leu Thr Leu Gln

1

5

10

15

Asp Leu Leu Gly Ile Leu Ser His Ser Ser Ala Ile Ser Asn Val Ala
 20 25 30
 Asn Gly Ile Tyr Val Glu Ser Glu Ile Leu Glu Val Gly Ser Trp Leu
 35 40 45
 Ser Ala Tyr Ala Ala Asn Lys Asp Glu Ile Phe Ser Gln Ile Ile Thr
 50 55 60
 Glu Leu Glu Asn Pro Tyr Gln Phe Gln Leu Glu Asn Asp Ile Gln Ala
 65 70 75 80
 Pro Ser Phe Ile Leu Tyr Ser Asn Glu Arg Ile Thr Ile Arg Leu Val
 85 90 95
 Met Trp Leu Pro Leu Gln Gly Lys Leu Asp Arg Thr Pro Tyr Ser Tyr
 100 105 110
 Glu Glu Ala His Asp His Asn Phe Asp Phe Trp Thr Val Asn Phe Phe
 115 120 125
 Gly Gly Gly Tyr Arg Thr Arg Leu Tyr Asp Tyr Asp Tyr Asp Lys Val
 130 135 140
 Ser Gly Val Asn Asn Glu Val Val Glu Leu Asn Cys Tyr Gly Asp Lys
 145 150 155 160
 Ile Leu Ser Pro Asn Thr Val Met Phe Tyr Phe Arg Ser Lys Asp Val
 165 170 175
 His Thr Gln Tyr Pro Pro Asp Glu Leu Ser Val Ser Leu Asn Leu Ile
 180 185 190
 Val Arg Pro Ile Lys Ser Lys His Gln Tyr Glu Phe Gln Ile Asp Ser
 195 200 205
 Asp Ala Leu Glu Gly Lys Ile Glu Ala Arg Ile Lys Lys Gly Arg Tyr
 210 215 220
 Glu Arg Tyr Ala Phe Gln Asn Val Leu Tyr Asn Gly Leu Leu Ser Leu
 225 230 235 240
 Glu Asn Glu Lys Ser Arg Gln Leu Val His Lys Val Ser Leu Cys Asn
 245 250 255
 His Arg Glu Glu Ile Arg Leu Ile Ala Tyr Glu Ala Leu Leu Lys His
 260 265 270

Ala Gln Lys Lys Gly Asn Val Ser Asp Ile Lys Ser Ile Ser Glu Gln
 275 280 285

Ala Phe Lys Asp Gln Ser Leu Tyr Ile Lys Asn Lys Ile Ser His Ser
 290 295 300

Ile Gly Ser Met Pro Cys Met Ser Pro Lys Pro Arg
 305 310 315

<210> 19

<211> 1347

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(1347)

<400> 19

atg aag gtt acg gtt ttt ggt att ggt tat gtg gga ctt gtt caa gct 48
 Met Lys Val Thr Val Phe Gly Ile Gly Tyr Val Gly Leu Val Gln Ala
 1 5 10 15

aca gtg ctt gcc gag gtg ggg cat gat gtc ctt tgt atc gat att gat 96
 Thr Val Leu Ala Glu Val Gly His Asp Val Leu Cys Ile Asp Ile Asp
 20 25 30

gct aat aaa gtt gcc gat ttg aaa aaa ggc cgt att gct att ttt gag 144
 Ala Asn Lys Val Ala Asp Leu Lys Lys Gly Arg Ile Ala Ile Phe Glu
 35 40 45

ccg ggc ttg gct ccg ttg gtc aaa gaa aac tat gag gca ggc aga tta 192
 Pro Gly Leu Ala Pro Leu Val Lys Glu Asn Tyr Glu Ala Gly Arg Leu
 50 55 60

cag ttt tca aca gat gcg caa gct ggt gtg gca cat ggc gtc att caa 240
 Gln Phe Ser Thr Asp Ala Gln Ala Gly Val Ala His Gly Val Ile Gln
 65 70 75 80

ttt att gct gtg ggt aca cct cct gat gaa gac ggt gct gcc gat ctt 288
 Phe Ile Ala Val Gly Thr Pro Pro Asp Glu Asp Gly Ala Ala Asp Leu
 85 90 95

aaa tat gtc ctt gat gtg gcc agt acc att ggc acg tat atg gac tca 336
 Lys Tyr Val Leu Asp Val Ala Ser Thr Ile Gly Thr Tyr Met Asp Ser

100	105	110	
cct aag gtc att atc gat aaa tct aca gtg ccc gtg ggg aca gcg gat			384
Pro Lys Val Ile Ile Asp Lys Ser Thr Val Pro Val Gly Thr Ala Asp			
115	120	125	
aaa gta cat caa gtt ata caa gct att ttg gag cag cgc ggt gag aag			432
Lys Val His Gln Val Ile Gln Ala Ile Leu Glu Gln Arg Gly Glu Lys			
130	135	140	
ata gat ttt agt gtg gta tca aat cct gag ttt tta aaa gag ggg gcc			480
Ile Asp Phe Ser Val Val Ser Asn Pro Glu Phe Leu Lys Glu Gly Ala			
145	150	155	160
gca gtt gct gat tgt aaa cgg cct gaa cgt att gtt att ggt att gat			528
Ala Val Ala Asp Cys Lys Arg Pro Glu Arg Ile Val Ile Gly Ile Asp			
165	170	175	
acg gat gac agt ggt gct cta gag tta atc agt gaa tta tac gaa cct			576
Thr Asp Asp Ser Gly Ala Leu Glu Leu Ile Ser Glu Leu Tyr Glu Pro			
180	185	190	
ttt aat cga aat cat gat cgt atg cta gta atg gat atc cgt agt gca			624
Phe Asn Arg Asn His Asp Arg Met Leu Val Met Asp Ile Arg Ser Ala			
195	200	205	
gaa ctg aca aag tat gct gca aac ggc atg ctg gca acg aaa ata agt			672
Glu Leu Thr Lys Tyr Ala Ala Asn Gly Met Leu Ala Thr Lys Ile Ser			
210	215	220	
ttc atg aat gag att gct aat att gct gag cga tta ggg gct gat atc			720
Phe Met Asn Glu Ile Ala Asn Ile Ala Glu Arg Leu Gly Ala Asp Ile			
225	230	235	240
gaa aaa gtt cga cag ggc atc ggt tcc gat tca cgt att gga tac cat			768
Glu Lys Val Arg Gln Gly Ile Gly Ser Asp Ser Arg Ile Gly Tyr His			
245	250	255	
ttc att tat tct ggt tgt ggt tat ggg ggg tct tgt ttc cca aaa gac			816
Phe Ile Tyr Ser Gly Cys Gly Tyr Gly Gly Ser Cys Phe Pro Lys Asp			
260	265	270	
atc caa gca tta att cgt act gca gaa gat aag ggt tat aag ccc cag			864
Ile Gln Ala Leu Ile Arg Thr Ala Glu Asp Lys Gly Tyr Lys Pro Gln			
275	280	285	
cta ttg cag gct gtc gag caa atc aat aat cag cag aag tat aag tta			912
Leu Leu Gln Ala Val Glu Gln Ile Asn Asn Gln Gln Lys Tyr Lys Leu			

290	295	300	
act gaa ttc att aaa agt cat ttt aat tcg cag tta gct gga aaa aca			960
Thr Glu Phe Ile Lys Ser His Phe Asn Ser Gln Leu Ala Gly Lys Thr			
305	310	315	320
ttt gct gtc tgg gga ttg gcc ttt aag ccc aac acc gat gat atg cgt			1008
Phe Ala Val Trp Gly Leu Ala Phe Lys Pro Asn Thr Asp Asp Met Arg			
325	330		335
gag gca ccg agc cgt gtg gta atg gaa tca ttg tgg gaa gcc ggg gct			1056
Glu Ala Pro Ser Arg Val Val Met Glu Ser Leu Trp Glu Ala Gly Ala			
340	345		350
aca att caa gca tac gat ccc gaa gca atg gat gag acg caa cgc att			1104
Thr Ile Gln Ala Tyr Asp Pro Glu Ala Met Asp Glu Thr Gln Arg Ile			
355	360		365
tat ggt gca aga gat gat ttg aga tta atg ggg act aaa gag tct gca			1152
Tyr Gly Ala Arg Asp Asp Leu Arg Leu Met Gly Thr Lys Glu Ser Ala			
370	375		380
tta cag gga gct gat gcc ttg att att tgt act gaa tgg caa agt ttt			1200
Leu Gln Gly Ala Asp Ala Leu Ile Ile Cys Thr Glu Trp Gln Ser Phe			
385	390		395
cgt gct cca gat ttt.gat atg atc aag tca agg tta aag cac cct gtt			1248
Arg Ala Pro Asp Phe Asp Met Ile Lys Ser Arg Leu Lys His Pro Val			
405	410		415
att ttt gat ggg cgt aat ttg tac gat cca gaa cgc cta aat agt cgt			1296
Ile Phe Asp Gly Arg Asn Leu Tyr Asp Pro Glu Arg Leu Asn Ser Arg			
420	425		430
ggg ttc act tat tat gga att ggg cgt ggt gtt tcg att aat cta tca			1344
Gly Phe Thr Tyr Tyr Gly Ile Gly Arg Gly Val Ser Ile Asn Leu Ser			
435	440		445
tag			1347

<210> 20

<211> 448

<212> PRT

<213> Yersinia pestis

<400> 20

Met Lys Val Thr Val Phe Gly Ile Gly Tyr Val Gly Leu Val Gln Ala
 1 5 10 15
 Thr Val Leu Ala Glu Val Gly His Asp Val Leu Cys Ile Asp Ile Asp
 20 25 30
 Ala Asn Lys Val Ala Asp Leu Lys Lys Gly Arg Ile Ala Ile Phe Glu
 35 40 45
 Pro Gly Leu Ala Pro Leu Val Lys Glu Asn Tyr Glu Ala Gly Arg Leu
 50 55 60
 Gln Phe Ser Thr Asp Ala Gln Ala Gly Val Ala His Gly Val Ile Gln
 65 70 75 80
 Phe Ile Ala Val Gly Thr Pro Pro Asp Glu Asp Gly Ala Ala Asp Leu
 85 90 95
 Lys Tyr Val Leu Asp Val Ala Ser Thr Ile Gly Thr Tyr Met Asp Ser
 100 105 110
 Pro Lys Val Ile Ile Asp Lys Ser Thr Val Pro Val Gly Thr Ala Asp
 115 120 125
 Lys Val His Gln Val Ile Gln Ala Ile Leu Glu Gln Arg Gly Glu Lys
 130 135 140
 Ile Asp Phe Ser Val Val Ser Asn Pro Glu Phe Leu Lys Glu Gly Ala
 145 150 155 160
 Ala Val Ala Asp Cys Lys Arg Pro Glu Arg Ile Val Ile Gly Ile Asp
 165 170 175
 Thr Asp Asp Ser Gly Ala Leu Glu Leu Ile Ser Glu Leu Tyr Glu Pro
 180 185 190
 Phe Asn Arg Asn His Asp Arg Met Leu Val Met Asp Ile Arg Ser Ala
 195 200 205
 Glu Leu Thr Lys Tyr Ala Ala Asn Gly Met Leu Ala Thr Lys Ile Ser
 210 215 220
 Phe Met Asn Glu Ile Ala Asn Ile Ala Glu Arg Leu Gly Ala Asp Ile
 225 230 235 240
 Glu Lys Val Arg Gln Gly Ile Gly Ser Asp Ser Arg Ile Gly Tyr His
 245 250 255

Phe Ile Tyr Ser Gly Cys Gly Tyr Gly Gly Ser Cys Phe Pro Lys Asp
 260 265 270

Ile Gln Ala Leu Ile Arg Thr Ala Glu Asp Lys Gly Tyr Lys Pro Gln
 275 280 285

Leu Leu Gln Ala Val Glu Gln Ile Asn Asn Gln Gln Lys Tyr Lys Leu
 290 295 300

Thr Glu Phe Ile Lys Ser His Phe Asn Ser Gln Leu Ala Gly Lys Thr
 305 310 315 320

Phe Ala Val Trp Gly Leu Ala Phe Lys Pro Asn Thr Asp Asp Met Arg
 325 330 335

Glu Ala Pro Ser Arg Val Val Met Glu Ser Leu Trp Glu Ala Gly Ala
 340 345 350

Thr Ile Gln Ala Tyr Asp Pro Glu Ala Met Asp Glu Thr Gln Arg Ile
 355 360 365

Tyr Gly Ala Arg Asp Asp Leu Arg Leu Met Gly Thr Lys Glu Ser Ala
 370 375 380

Leu Gln Gly Ala Asp Ala Leu Ile Ile Cys Thr Glu Trp Gln Ser Phe
 385 390 395 400

Arg Ala Pro Asp Phe Asp Met Ile Lys Ser Arg Leu Lys His Pro Val
 405 410 415

Ile Phe Asp Gly Arg Asn Leu Tyr Asp Pro Glu Arg Leu Asn Ser Arg
 420 425 430

Gly Phe Thr Tyr Tyr Gly Ile Gly Arg Gly Val Ser Ile Asn Leu Ser
 435 440 445

<210> 21

<211> 822

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(822)

<400> 21

atg aag aat att aag gtt tat caa tat atc aag tgg gtc att atg cca 48
 Met Lys Asn Ile Lys Val Tyr Gln Tyr Ile Lys Trp Val Ile Met Pro
 1 5 10 15

act att gtg ctg tta atg tgg caa atg ctc gcc ata tcg ggc tgg ata 96
 Thr Ile Val Leu Leu Met Trp Gln Met Leu Ala Ile Ser Gly Trp Ile
 20 25 30

caa ccc aca ata ctt cca tca cca gta gcc gtt gtg gtg cgc tgg ttc 144
 Gln Pro Thr Ile Leu Pro Ser Pro Val Ala Val Val Val Arg Trp Phe
 35 40 45

gat tat ttc tta ccc tat gaa gcc tat aac cca gaa aca tca aac tgg 192
 Asp Tyr Phe Leu Pro Tyr Glu Ala Tyr Asn Pro Glu Thr Ser Asn Trp
 50 55 60

ctg atg tgg agt ctt tca ggg gag tta ctg cat gat gcc tgg gcg agt 240
 Leu Met Trp Ser Leu Ser Gly Glu Leu Leu His Asp Ala Trp Ala Ser
 65 70 75 80

atc tac cgc gta att att ggt ttt cta atc ggt gct ctt ctt gct cta 288
 Ile Tyr Arg Val Ile Ile Gly Phe Leu Ile Gly Ala Leu Leu Ala Leu
 85 90 95

cca tta gga tta tgg gtg ggt tcc agt aaa att ggc aat gac cta atg 336
 Pro Leu Gly Leu Trp Val Gly Ser Ser Lys Ile Gly Asn Asp Leu Met
 100 105 110

aac cct tta att cag ttt ctt cgc ccc att ccg cca att gca tat att 384
 Asn Pro Leu Ile Gln Phe Leu Arg Pro Ile Pro Pro Ile Ala Tyr Ile
 115 120 125

cca tta gcg atg ctg tgg ttc ggc ctg ggg aat ccg ccg gca ttt ttt 432
 Pro Leu Ala Met Leu Trp Phe Gly Leu Gly Asn Pro Pro Ala Phe Phe
 130 135 140

ttg ata agt ata ggg gct ttt ttc cca ata ctg att aat acc atc gcg 480
 Leu Ile Ser Ile Gly Ala Phe Phe Pro Ile Leu Ile Asn Thr Ile Ala
 145 150 155 160

ggg gtc cgt aat gtg gat ggc ata tat atc ctg gct gca cgc aat cta 528
 Gly Val Arg Asn Val Asp Gly Ile Tyr Ile Leu Ala Ala Arg Asn Leu
 165 170 175

ggc gca ggt caa gcc acg atg ttt cgc cga att att ctt ccg gcg gcc 576
 Gly Ala Gly Gln Ala Thr Met Phe Arg Arg Ile Ile Leu Pro Ala Ala
 180 185 190

act cct tat att ctt aca ggg atg cga gtt ggt ata ggg acc gcg ttt 624
 Thr Pro Tyr Ile Leu Thr Gly Met Arg Val Gly Ile Gly Thr Ala Phe
 195 200 205

att tgc gtg att gtg gca gaa atg atc gcc gtt aat agc ggt gtt ggc 672
 Ile Cys Val Ile Val Ala Glu Met Ile Ala Val Asn Ser Gly Val Gly
 210 215 220

tac cga att ctg gaa gcg cgc gaa tat atg tgg tcc gat aaa gta ata 720
 Tyr Arg Ile Leu Glu Ala Arg Glu Tyr Met Trp Ser Asp Lys Val Ile
 225 230 235 240

gca ggc atg ttc aca att ggt ttt ctt ggc ctg gtc att gat tta tgc 768
 Ala Gly Met Phe Thr Ile Gly Phe Leu Gly Leu Val Ile Asp Leu Cys
 245 250 255

atg gat cgc ctg aat cgg cgt ctt tta cgc tgg cac aga gga ata ggc 816
 Met Asp Arg Leu Asn Arg Arg Leu Leu Arg Trp His Arg Gly Ile Gly
 260 265 270

aac tga 822
 Asn

<210> 22

<211> 273

<212> PRT

<213> Yersinia pestis

<400> 22

Met Lys Asn Ile Lys Val Tyr Gln Tyr Ile Lys Trp Val Ile Met Pro
 1 5 10 15

Thr Ile Val Leu Leu Met Trp Gln Met Leu Ala Ile Ser Gly Trp Ile
 20 25 30

Gln Pro Thr Ile Leu Pro Ser Pro Val Ala Val Val Val Arg Trp Phe
 35 40 45

Asp Tyr Phe Leu Pro Tyr Glu Ala Tyr Asn Pro Glu Thr Ser Asn Trp
 50 55 60

Leu Met Trp Ser Leu Ser Gly Glu Leu Leu His Asp Ala Trp Ala Ser
 65 70 75 80

Ile Tyr Arg Val Ile Ile Gly Phe Leu Ile Gly Ala Leu Leu Ala Leu
 85 90 95

Pro Leu Gly Leu Trp Val Gly Ser Ser Lys Ile Gly Asn Asp Leu Met
 100 105 110

Asn Pro Leu Ile Gln Phe Leu Arg Pro Ile Pro Pro Ile Ala Tyr Ile
 115 120 125

Pro Leu Ala Met Leu Trp Phe Gly Leu Gly Asn Pro Pro Ala Phe Phe
 130 135 140

Leu Ile Ser Ile Gly Ala Phe Phe Pro Ile Leu Ile Asn Thr Ile Ala
 145 150 155 160

Gly Val Arg Asn Val Asp Gly Ile Tyr Ile Leu Ala Ala Arg Asn Leu
 165 170 175

Gly Ala Gly Gln Ala Thr Met Phe Arg Arg Ile Ile Leu Pro Ala Ala
 180 185 190

Thr Pro Tyr Ile Leu Thr Gly Met Arg Val Gly Ile Gly Thr Ala Phe
 195 200 205

Ile Cys Val Ile Val Ala Glu Met Ile Ala Val Asn Ser Gly Val Gly
 210 215 220

Tyr Arg Ile Leu Glu Ala Arg Glu Tyr Met Trp Ser Asp Lys Val Ile
 225 230 235 240

Ala Gly Met Phe Thr Ile Gly Phe Leu Gly Leu Val Ile Asp Leu Cys
 245 250 255

Met Asp Arg Leu Asn Arg Arg Leu Leu Arg Trp His Arg Gly Ile Gly
 260 265 270

Asn

<210> 23

<211> 891

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1)..(891)

<400> 23

atg agc cac cct gtt ttt gtc cgc cct gag ctg gta gtg gat aac gtc 48

Met	Ser	His	Pro	Val	Phe	Val	Arg	Pro	Glu	Leu	Val	Val	Asp	Asn	Val		
1				5					10					15			
act gtc act tat aac aat ggt cat act gcc att tat gac gcc agc ttt																	96
Thr Val Thr Tyr Asn Asn Gly His Thr Ala Ile Tyr Asp Ala Ser Phe																	
				20				25					30				
tca cta acg ggt ggg acg atc tgt gca ctg gta ggt gtt aat ggc agc																	144
Ser Leu Thr Gly Gly Thr Ile Cys Ala Leu Val Gly Val Asn Gly Ser																	
				35				40					45				
ggt aaa tcg acc tta ttt aaa agc att atg ggg tta gtc aag ccc agt																	192
Gly Lys Ser Thr Leu Phe Lys Ser Ile Met Gly Leu Val Lys Pro Ser																	
				50				55					60				
gtg ggc aaa gtg gaa ctg agt cac aaa cct atc agt cat gca cta aaa																	240
Val Gly Lys Val Glu Leu Ser His Lys Pro Ile Ser His Ala Leu Lys																	
				65				70					75				80
caa aat acg att gct tat gta cca cag aca gaa gat gtc gat tgg aac																	288
Gln Asn Thr Ile Ala Tyr Val Pro Gln Thr Glu Asp Val Asp Trp Asn																	
								85					90				95
ttc cct gtg ctt gtg gaa gat gtc gtg atg atg ggc cgt tac ggt aaa																	336
Phe Pro Val Leu Val Glu Asp Val Val Met Met Gly Arg Tyr Gly Lys																	
				100				105					110				
atg aat ttt cta cga att ccc agt cgt gaa gac aaa gcc att gtg aat																	384
Met Asn Phe Leu Arg Ile Pro Ser Arg Glu Asp Lys Ala Ile Val Asn																	
				115				120					125				
aaa tcc att gaa cga gtt ggg tta acg gca ttg cgt tca cgg caa att																	432
Lys Ser Ile Glu Arg Val Gly Leu Thr Ala Leu Arg Ser Arg Gln Ile																	
				130				135					140				
ggt gaa ctg tct ggt ggc cag aaa aaa cgt gtt ttc ttg gcc cga gcc																	480
Gly Glu Leu Ser Gly Gly Gln Lys Lys Arg Val Phe Leu Ala Arg Ala																	
				145				150					155				160
ctt gcc caa caa ggc aca ctc tta cta ctg gat gag cca ttt acc ggc																	528
Leu Ala Gln Gln Gly Thr Leu Leu Leu Leu Asp Glu Pro Phe Thr Gly																	
								165					170				175
gtt gac gtc aaa act gaa aat gcc att att gag tta ctg caa tct cta																	576
Val Asp Val Lys Thr Glu Asn Ala Ile Ile Glu Leu Leu Gln Ser Leu																	
				180				185					190				
cgt gac gaa ggc cat ctg att ctg gtt tca act cat aac cta ggc agc																	624

Arg Asp Glu Gly His Leu Ile Leu Val Ser Thr His Asn Leu Gly Ser
 195 200 205

 gtg ccg gaa ttt tgt gat cac gtc atc cta att aat cag acg gtg ctg 672
 Val Pro Glu Phe Cys Asp His Val Ile Leu Ile Asn Gln Thr Val Leu
 210 215 220

 gcc gcg ggc cca att gaa acg aca ttt acc cag aaa aac ctc gag atg 720
 Ala Ala Gly Pro Ile Glu Thr Thr Phe Thr Gln Lys Asn Leu Glu Met
 225 230 235 240

 acc ttt ggc ggg gta ttg cgc cat atc aat ctg tcg ggg acg gca ctg 768
 Thr Phe Gly Gly Val Leu Arg His Ile Asn Leu Ser Gly Thr Ala Leu
 245 250 255

 cat gat gat aat gat ccg cgc acc gtc acc gta ata act gat gat gaa 816
 His Asp Asp Asn Asp Pro Arg Thr Val Thr Val Ile Thr Asp Asp Glu
 260 265 270

 cgc ccc gca gta ttt tat ggt cat act aaa aat gat ccg cct gca caa 864
 Arg Pro Ala Val Phe Tyr Gly His Thr Lys Asn Asp Pro Pro Ala Gln
 275 280 285

 agc cag tca aag gag caa aat tcc tga 891
 Ser Gln Ser Lys Glu Gln Asn Ser
 290 295

<210> 24

<211> 296

<212> PRT

<213> Yersinia pestis

<400> 24

Met Ser His Pro Val Phe Val Arg Pro Glu Leu Val Val Asp Asn Val
 1 5 10 15

Thr Val Thr Tyr Asn Asn Gly His Thr Ala Ile Tyr Asp Ala Ser Phe
 20 25 30

Ser Leu Thr Gly Gly Thr Ile Cys Ala Leu Val Gly Val Asn Gly Ser
 35 40 45

Gly Lys Ser Thr Leu Phe Lys Ser Ile Met Gly Leu Val Lys Pro Ser
 50 55 60

Val Gly Lys Val Glu Leu Ser His Lys Pro Ile Ser His Ala Leu Lys
 65 70 75 80

Gln Asn Thr Ile Ala Tyr Val Pro Gln Thr Glu Asp Val Asp Trp Asn
 85 90 95

 Phe Pro Val Leu Val Glu Asp Val Val Met Met Gly Arg Tyr Gly Lys
 100 105 110

 Met Asn Phe Leu Arg Ile Pro Ser Arg Glu Asp Lys Ala Ile Val Asn
 115 120 125

 Lys Ser Ile Glu Arg Val Gly Leu Thr Ala Leu Arg Ser Arg Gln Ile
 130 135 140

 Gly Glu Leu Ser Gly Gly Gln Lys Lys Arg Val Phe Leu Ala Arg Ala
 145 150 155 160

 Leu Ala Gln Gln Gly Thr Leu Leu Leu Leu Asp Glu Pro Phe Thr Gly
 165 170 175

 Val Asp Val Lys Thr Glu Asn Ala Ile Ile Glu Leu Leu Gln Ser Leu
 180 185 190

 Arg Asp Glu Gly His Leu Ile Leu Val Ser Thr His Asn Leu Gly Ser
 195 200 205

 Val Pro Glu Phe Cys Asp His Val Ile Leu Ile Asn Gln Thr Val Leu
 210 215 220

 Ala Ala Gly Pro Ile Glu Thr Thr Phe Thr Gln Lys Asn Leu Glu Met
 225 230 235 240

 Thr Phe Gly Gly Val Leu Arg His Ile Asn Leu Ser Gly Thr Ala Leu
 245 250 255

 His Asp Asp Asn Asp Pro Arg Thr Val Thr Val Ile Thr Asp Asp Glu
 260 265 270

 Arg Pro Ala Val Phe Tyr Gly His Thr Lys Asn Asp Pro Pro Ala Gln
 275 280 285

 Ser Gln Ser Lys Glu Gln Asn Ser
 290 295

<210> 25

<211> 213

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1)..(213)

<400> 25

atg agt ttc aag tca ata aat aaa aac gca gat ttg tac gtg act tgc 48
 Met Ser Phe Lys Ser Ile Asn Lys Asn Ala Asp Leu Tyr Val Thr Cys
 1 5 10 15

agt ggc ctg gaa gag gcg ggg tcc atg gac ggg ccg agt cac gaa ggc 96
 Ser Gly Leu Glu Glu Ala Gly Ser Met Asp Gly Pro Ser His Glu Gly
 20 25 30

aac cag cac aca ggc agc ttg aag cct gat ggg tat att atc att caa 144
 Asn Gln His Thr Gly Ser Leu Lys Pro Asp Gly Tyr Ile Ile Ile Gln
 35 40 45

gaa aat gat tta att tct gga ttt gat aac aca gtc ggc ata gct aat 192
 Glu Asn Asp Leu Ile Ser Gly Phe Asp Asn Thr Val Gly Ile Ala Asn
 50 55 60

aac cgt ttc agg aga tgt taa 213
 Asn Arg Phe Arg Arg Cys
 65 70

<210> 26

<211> 70

<212> PRT

<213> *Yersinia pestis*

<400> 26

Met Ser Phe Lys Ser Ile Asn Lys Asn Ala Asp Leu Tyr Val Thr Cys
 1 5 10 15

Ser Gly Leu Glu Glu Ala Gly Ser Met Asp Gly Pro Ser His Glu Gly
 20 25 30

Asn Gln His Thr Gly Ser Leu Lys Pro Asp Gly Tyr Ile Ile Ile Gln
 35 40 45

Glu Asn Asp Leu Ile Ser Gly Phe Asp Asn Thr Val Gly Ile Ala Asn
 50 55 60

Asn Arg Phe Arg Arg Cys
 65 70

<210> 27

<211> 657

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1)..(657)

<400> 27

atg cag aaa gaa aag ctt tcc gct ttg atg gat gga gaa act ctc gat 48
 Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Thr Leu Asp
 1 5 10 15

agc gag ctg ctg ggg att tta tcg aaa gat aag gcg tta cag caa agc 96
 Ser Glu Leu Leu Gly Ile Leu Ser Lys Asp Lys Ala Leu Gln Gln Ser
 20 25 30

tgg cag agc tac cat tta atc cgt gac act cta cgc gga gac gtt ggc 144
 Trp Gln Ser Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
 35 40 45

aat gtt tta cat ctg gat att gct agt cgt gta gca gaa gcg ctc aag 192
 Asn Val Leu His Leu Asp Ile Ala Ser Arg Val Ala Glu Ala Leu Lys
 50 55 60

aac gag cca gcg cgc ttg att cct att gct ata cct gaa tct cag cca 240
 Asn Glu Pro Ala Arg Leu Ile Pro Ile Ala Ile Pro Glu Ser Gln Pro
 65 70 75 80

cag cca cat ctt tgg cag aaa atg cct ttc tgg caa aaa gtc cgt cca 288
 Gln Pro His Leu Trp Gln Lys Met Pro Phe Trp Gln Lys Val Arg Pro
 85 90 95

tgg gcc agt cag att act cag gtg gga atg gcc gct tgt gtt tct ctc 336
 Trp Ala Ser Gln Ile Thr Gln Val Gly Met Ala Ala Cys Val Ser Leu
 100 105 110

gct gtc att gtt ggt gtt caa caa tat aac caa ccg gca caa aat tat 384
 Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ala Gln Asn Tyr
 115 120 125

tta caa cct gaa tca ccg gcg ttt aat acc ttg cca atg atg ggt aaa 432
 Leu Gln Pro Glu Ser Pro Ala Phe Asn Thr Leu Pro Met Met Gly Lys
 130 135 140

gca tca cca gtc agt ttt ggt gtc cct gct gat ggt tct ttt ggt act 480
 Ala Ser Pro Val Ser Phe Gly Val Pro Ala Asp Gly Ser Phe Gly Thr
 145 150 155 160

aat caa cag aat cag gtt caa gag cag cgt cgg cgc gtc aac atg atg 528
 Asn Gln Gln Asn Gln Val Gln Glu Gln Arg Arg Arg Val Asn Met Met
 165 170 175

act caa ttg caa gat ttt gaa ttg caa cgt cgt ttg cca caa act gat 576
 Thr Gln Leu Gln Asp Phe Glu Leu Gln Arg Arg Leu Pro Gln Thr Asp
 180 185 190

gta ttg cag cag cct tca gat tca acg caa gcc gca att caa gtc cct 624
 Val Leu Gln Gln Pro Ser Asp Ser Thr Gln Ala Ala Ile Gln Val Pro
 195 200 205

gga act caa tcc tta gga atg cag cag cag taa 657
 Gly Thr Gln Ser Leu Gly Met Gln Gln Gln
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<210> 28

<211> 218

<212> PRT

<213> Yersinia pestis

<400> 28

Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Thr Leu Asp
 1 5 10 15

Ser Glu Leu Leu Gly Ile Leu Ser Lys Asp Lys Ala Leu Gln Gln Ser
 20 25 30

Trp Gln Ser Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
 35 40 45

Asn Val Leu His Leu Asp Ile Ala Ser Arg Val Ala Glu Ala Leu Lys
 50 55 60

Asn Glu Pro Ala Arg Leu Ile Pro Ile Ala Ile Pro Glu Ser Gln Pro
 65 70 75 80

Gln Pro His Leu Trp Gln Lys Met Pro Phe Trp Gln Lys Val Arg Pro
 85 90 95

Trp Ala Ser Gln Ile Thr Gln Val Gly Met Ala Ala Cys Val Ser Leu
 100 105 110

Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ala Gln Asn Tyr
 115 120 125

Leu Gln Pro Glu Ser Pro Ala Phe Asn Thr Leu Pro Met Met Gly Lys
 130 135 140

Ala Ser Pro Val Ser Phe Gly Val Pro Ala Asp Gly Ser Phe Gly Thr
 145 150 155 160

Asn Gln Gln Asn Gln Val Gln Glu Gln Arg Arg Arg Val Asn Met Met
 165 170 175

Thr Gln Leu Gln Asp Phe Glu Leu Gln Arg Arg Leu Pro Gln Thr Asp
 180 185 190

Val Leu Gln Gln Pro Ser Asp Ser Thr Gln Ala Ala Ile Gln Val Pro
 195 200 205

Gly Thr Gln Ser Leu Gly Met Gln Gln Gln
 210 215

<210> 29

<211> 1413

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1)..(1413)

<400> 29

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 Leu Leu Met Leu Leu Pro Val Ile Met Ala Gly Gly Ala Gly Ser Arg
 1 5 10 15

ttg tgg cca tta tcc cga gct ctt tat cct aaa caa ttt cta gcg cta 96
 Leu Trp Pro Leu Ser Arg Ala Leu Tyr Pro Lys Gln Phe Leu Ala Leu
 20 25 30

acg tca gat ttg acg atg cta caa gaa acc cta ttg cgt ctg gac ggc 144
 Thr Ser Asp Leu Thr Met Leu Gln Glu Thr Leu Leu Arg Leu Asp Gly
 35 40 45

ctt ccc cac ctt gca cca tta gtg att tgt aac gaa gaa cat cgc ttt 192
 Leu Pro His Leu Ala Pro Leu Val Ile Cys Asn Glu Glu His Arg Phe

50	55	60	
att atc gca gaa cag tta cgt cag aaa aat ctg gtg cat agc gga ata			240
Ile Ile Ala Glu Gln Leu Arg Gln Lys Asn Leu Val His Ser Gly Ile			
65	70	75	80
gtc ttg gaa cct gtt ggg cgc aat acc gcg cca gct ata gca ttg gct			288
Val Leu Glu Pro Val Gly Arg Asn Thr Ala Pro Ala Ile Ala Leu Ala			
	85	90	95
gcc tta cga gca aca atg agt ggg gat gat cct cta tta ttg gta tta			336
Ala Leu Arg Ala Thr Met Ser Gly Asp Asp Pro Leu Leu Leu Val Leu			
	100	105	110
gca gcc gat cac gtg att cag gat aaa ctt gca ttt att cgt gcc gtc			384
Ala Ala Asp His Val Ile Gln Asp Lys Leu Ala Phe Ile Arg Ala Val			
	115	120	125
caa cgt gct gaa ccg ctt gct gaa gcg gga aaa ttg gtt act ttt gga			432
Gln Arg Ala Glu Pro Leu Ala Glu Ala Gly Lys Leu Val Thr Phe Gly			
	130	135	140
atc gtg cca aag agt ccg gaa aca gga tat gga tat att cgc caa ggg			480
Ile Val Pro Lys Ser Pro Glu Thr Gly Tyr Gly Tyr Ile Arg Gln Gly			
145	150	155	160
aag caa gtc gta gat ggc gct tat cag gtt gct gct ttt gtt gag aag			528
Lys Gln Val Val Asp Gly Ala Tyr Gln Val Ala Ala Phe Val Glu Lys			
	165	170	175
cca gat ctg att act gca gag cgg tat ttg gct tcg ggt gac tat tat			576
Pro Asp Leu Ile Thr Ala Glu Arg Tyr Leu Ala Ser Gly Asp Tyr Tyr			
	180	185	190
tgg aat agc ggt atg ttt gta ttt aaa gca tct cgc tat cta cag gaa			624
Trp Asn Ser Gly Met Phe Val Phe Lys Ala Ser Arg Tyr Leu Gln Glu			
	195	200	205
tta gat cta cat cgt ccg gat att ttg gct gcc tgc aag caa gcc att			672
Leu Asp Leu His Arg Pro Asp Ile Leu Ala Ala Cys Lys Gln Ala Ile			
	210	215	220
gct ggt caa cat act gat tta gat ttt att cgt ctc aat gaa gaa gct			720
Ala Gly Gln His Thr Asp Leu Asp Phe Ile Arg Leu Asn Glu Glu Ala			
225	230	235	240
ttc tct agt tgc cct gat gaa tct atc gac tat gct gtg atg gaa aaa			768
Phe Ser Ser Cys Pro Asp Glu Ser Ile Asp Tyr Ala Val Met Glu Lys			

	245	250	255	
act agc gat gcc gtt gta gtg cca ctg gat gca cag tgg aat gat gtt				816
Thr Ser Asp Ala Val Val Val Pro Leu Asp Ala Gln Trp Asn Asp Val				
	260	265	270	
ggg tgc tgg tca gcg ctt tgg gaa att aat act aaa gat gac cat ggt				864
Gly Cys Trp Ser Ala Leu Trp Glu Ile Asn Thr Lys Asp Asp His Gly				
	275	280	285	
aat gtt att cgt ggt gat gta tta ata gaa gat act aat aat agc tac				912
Asn Val Ile Arg Gly Asp Val Leu Ile Glu Asp Thr Asn Asn Ser Tyr				
	290	295	300	
gtt tat tct caa aat agg ctc att gca act gta ggc att aat gat ttg				960
Val Tyr Ser Gln Asn Arg Leu Ile Ala Thr Val Gly Ile Asn Asp Leu				
	305	310	315	320
gtt att gtt gaa act aaa gat gcc att tta gtt gct cat aaa gat aaa				1008
Val Ile Val Glu Thr Lys Asp Ala Ile Leu Val Ala His Lys Asp Lys				
	325	330	335	
gta caa aat gtt aaa ggg atc gtt gga cag ctt aag ctt gaa tct cga				1056
Val Gln Asn Val Lys Gly Ile Val Gly Gln Leu Lys Leu Glu Ser Arg				
	340	345	350	
tgt gaa tat cta cag cac cgg gaa gtc tat cgc cct tgg ggt tcg cat				1104
Cys Glu Tyr Leu Gln His Arg Glu Val Tyr Arg Pro Trp Gly Ser His				
	355	360	365	
gat gct att gct gaa ggt gtt cgc tac cat gtc caa cat gta acg gtg				1152
Asp Ala Ile Ala Glu Gly Val Arg Tyr His Val Gln His Val Thr Val				
	370	375	380	
aaa cca ggt caa cgt att gct act caa att cat tat cac aga gcg gaa				1200
Lys Pro Gly Gln Arg Ile Ala Thr Gln Ile His Tyr His Arg Ala Glu				
	385	390	395	400
cat tgg att gtg gtt tct ggc att gcc aaa gta cat tat gga aaa gaa				1248
His Trp Ile Val Val Ser Gly Ile Ala Lys Val His Tyr Gly Lys Glu				
	405	410	415	
act tat ttg gtt aat gag aat gaa tcc act tat att ccc gtc ggc att				1296
Thr Tyr Leu Val Asn Glu Asn Glu Ser Thr Tyr Ile Pro Val Gly Ile				
	420	425	430	
gct cat tct att gaa aat cca ggt cag atc cct ctg gaa ata ata gag				1344
Ala His Ser Ile Glu Asn Pro Gly Gln Ile Pro Leu Glu Ile Ile Glu				

435

440

445

gtt cat act ggt aat tac att tca gaa gat gat gtg gaa cga atc gat 1392
 Val His Thr Gly Asn Tyr Ile Ser Glu Asp Asp Val Glu Arg Ile Asp
 450 455 460

gat tta ggt gta ggg tat taa 1413
 Asp Leu Gly Val Gly Tyr
 465 470

<210> 30

<211> 470

<212> PRT

<213> Yersinia pestis

<400> 30

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Leu Trp Pro Leu Ser Arg Ala Leu Tyr Pro Lys Gln Phe Leu Ala Leu
 20 25 30

Thr Ser Asp Leu Thr Met Leu Gln Glu Thr Leu Leu Arg Leu Asp Gly
 35 40 45

Leu Pro His Leu Ala Pro Leu Val Ile Cys Asn Glu Glu His Arg Phe
 50 55 60

Ile Ile Ala Glu Gln Leu Arg Gln Lys Asn Leu Val His Ser Gly Ile
 65 70 75 80

Val Leu Glu Pro Val Gly Arg Asn Thr Ala Pro Ala Ile Ala Leu Ala
 85 90 95

Ala Leu Arg Ala Thr Met Ser Gly Asp Asp Pro Leu Leu Leu Val Leu
 100 105 110

Ala Ala Asp His Val Ile Gln Asp Lys Leu Ala Phe Ile Arg Ala Val
 115 120 125

Gln Arg Ala Glu Pro Leu Ala Glu Ala Gly Lys Leu Val Thr Phe Gly
 130 135 140

Ile Val Pro Lys Ser Pro Glu Thr Gly Tyr Gly Tyr Ile Arg Gln Gly
 145 150 155 160

Lys Gln Val Val Asp Gly Ala Tyr Gln Val Ala Ala Phe Val Glu Lys

	165	170	175
Pro Asp Leu Ile Thr Ala Glu Arg Tyr Leu Ala Ser Gly Asp Tyr Tyr			
	180	185	190
Trp Asn Ser Gly Met Phe Val Phe Lys Ala Ser Arg Tyr Leu Gln Glu			
	195	200	205
Leu Asp Leu His Arg Pro Asp Ile Leu Ala Ala Cys Lys Gln Ala Ile			
	210	215	220
Ala Gly Gln His Thr Asp Leu Asp Phe Ile Arg Leu Asn Glu Glu Ala			
	225	230	235
Phe Ser Ser Cys Pro Asp Glu Ser Ile Asp Tyr Ala Val Met Glu Lys			
	245	250	255
Thr Ser Asp Ala Val Val Val Pro Leu Asp Ala Gln Trp Asn Asp Val			
	260	265	270
Gly Cys Trp Ser Ala Leu Trp Glu Ile Asn Thr Lys Asp Asp His Gly			
	275	280	285
Asn Val Ile Arg Gly Asp Val Leu Ile Glu Asp Thr Asn Asn Ser Tyr			
	290	295	300
Val Tyr Ser Gln Asn Arg Leu Ile Ala Thr Val Gly Ile Asn Asp Leu			
	305	310	315
Val Ile Val Glu Thr Lys Asp Ala Ile Leu Val Ala His Lys Asp Lys			
	325	330	335
Val Gln Asn Val Lys Gly Ile Val Gly Gln Leu Lys Leu Glu Ser Arg			
	340	345	350
Cys Glu Tyr Leu Gln His Arg Glu Val Tyr Arg Pro Trp Gly Ser His			
	355	360	365
Asp Ala Ile Ala Glu Gly Val Arg Tyr His Val Gln His Val Thr Val			
	370	375	380
Lys Pro Gly Gln Arg Ile Ala Thr Gln Ile His Tyr His Arg Ala Glu			
	385	390	395
His Trp Ile Val Val Ser Gly Ile Ala Lys Val His Tyr Gly Lys Glu			
	405	410	415
Thr Tyr Leu Val Asn Glu Asn Glu Ser Thr Tyr Ile Pro Val Gly Ile			

420 425 430
 Ala His Ser Ile Glu Asn Pro Gly Gln Ile Pro Leu Glu Ile Ile Glu
 435 440 445
 Val His Thr Gly Asn Tyr Ile Ser Glu Asp Asp Val Glu Arg Ile Asp
 450 455 460
 Asp Leu Gly Val Gly Tyr
 465 470

<210> 31
 <211> 1014
 <212> DNA
 <213> Yersinia pestis

<220>
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 <222> (1)..(1014)

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 ggg gta act gtc tat ttc tgc gag tta gtg agt cga ctt cct gca aca 96
 Gly Val Thr Val Tyr Phe Ser Glu Leu Val Ser Arg Leu Pro Ala Thr
 20 25 30
 gat ttt tat tgg tac tca tac gca gat gaa ata tct ggt ttc ggt gtt 144
 Asp Phe Tyr Trp Tyr Ser Tyr Ala Asp Glu Ile Ser Gly Phe Gly Val
 35 40 45
 ggt aat gtt aaa ata aaa tct aga ctt tta gag cga tat agg aat ttc 192
 Gly Asn Val Lys Ile Lys Ser Arg Leu Leu Glu Arg Tyr Arg Asn Phe
 50 55 60
 tca tta gat act att aat tat aat tct ctt tct gta ttt cat tca tca 240
 Ser Leu Asp Thr Ile Asn Tyr Asn Ser Leu Ser Val Phe His Ser Ser
 65 70 75 80
 tat tac cga tta cca gat ttt gac att ccg ata gtt aca aca gtt cat 288
 Tyr Tyr Arg Leu Pro Asp Phe Asp Ile Pro Ile Val Thr Thr Val His
 85 90 95
 gat ttc aca tat gaa aag ttt gtt aat ggc cct gca aaa tgg gtg cat 336

Asp Phe Thr Tyr Glu Lys Phe Val Asn Gly Pro Ala Lys Trp Val His	
100 105 110	
tcc tgg cag aaa aac cgt gcg gtt aac aat agt gat tta att att tgt	384
Ser Trp Gln Lys Asn Arg Ala Val Asn Asn Ser Asp Leu Ile Ile Cys	
115 120 125	
gtt tcg gaa aat aca gct aaa gat ttg caa atg tat tgc tca gtt cct	432
Val Ser Glu Asn Thr Ala Lys Asp Leu Gln Met Tyr Cys Ser Val Pro	
130 135 140	
agc aat aaa atc aga gtg ata tat aac ggt gtg tca gat aaa tat cat	480
Ser Asn Lys Ile Arg Val Ile Tyr Asn Gly Val Ser Asp Lys Tyr His	
145 150 155 160	
tat att aag ggt gtt aaa ata acc aca aat aaa gtt att ttt gtt ggt	528
Tyr Ile Lys Gly Val Lys Ile Thr Thr Asn Lys Val Ile Phe Val Gly	
165 170 175	
gca cgt ggt ggt tat aag aat ttt gac att gca gtg aaa gca ata tca	576
Ala Arg Gly Gly Tyr Lys Asn Phe Asp Ile Ala Val Lys Ala Ile Ser	
180 185 190	
aaa aca cct cac ctg gaa tta tca gtt gta ggt gga ggg gca ttc act	624
Lys Thr Pro His Leu Glu Leu Ser Val Val Gly Gly Gly Ala Phe Thr	
195 200 205	
agt aaa gaa ctg tca cta ctg aat cac tat tta cct ggt cgc tac cat	672
Ser Lys Glu Leu Ser Leu Leu Asn His Tyr Leu Pro Gly Arg Tyr His	
210 215 220	
gga tta ggt cgc ctt agt gat gag gct ttg aat gag gca tat aat tca	720
Gly Leu Gly Arg Leu Ser Asp Glu Ala Leu Asn Glu Ala Tyr Asn Ser	
225 230 235 240	
gct tat gcg ctg ctt tac cca tct agc tat gag ggt ttt ggt att cca	768
Ala Tyr Ala Leu Leu Tyr Pro Ser Ser Tyr Glu Gly Phe Gly Ile Pro	
245 250 255	
ata tta gaa gcg atg agt gca gga tgt ccc gta ata tct gtt aat gta	816
Ile Leu Glu Ala Met Ser Ala Gly Cys Pro Val Ile Ser Val Asn Val	
260 265 270	
tct tct ata cct gag gtc gca ggt gat gcc gct ata tta gtg caa aaa	864
Ser Ser Ile Pro Glu Val Ala Gly Asp Ala Ala Ile Leu Val Gln Lys	
275 280 285	
ccg act att gat gaa cta gtt gac ggc ttg ctt gcc gta gaa agt gaa	912

Pro Thr Ile Asp Glu Leu Val Asp Gly Leu Leu Ala Val Glu Ser Glu
 290 295 300

agg tct aaa ctt att ggc tat ggc atg aag caa gcg gct aaa ttc tca 960
 Arg Ser Lys Leu Ile Gly Tyr Gly Met Lys Gln Ala Ala Lys Phe Ser
 305 310 315 320

tgg gat aag tgt tat caa gaa acc tta gat gtt tat aaa gaa ttg aac 1008
 Trp Asp Lys Cys Tyr Gln Glu Thr Leu Asp Val Tyr Lys Glu Leu Asn
 325 330 335

aaa taa 1014
 Lys

<210> 32

<211> 337

<212> PRT

<213> Yersinia pestis

<400> 32

Met Lys Ile Ile Tyr Asp Gly Ile Ile Asn Ser Leu Gln Asn Met Gly
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Gly Val Thr Val Tyr Phe Ser Glu Leu Val Ser Arg Leu Pro Ala Thr
 20 25 30

Asp Phe Tyr Trp Tyr Ser Tyr Ala Asp Glu Ile Ser Gly Phe Gly Val
 35 40 45

Gly Asn Val Lys Ile Lys Ser Arg Leu Leu Glu Arg Tyr Arg Asn Phe
 50 55 60

Ser Leu Asp Thr Ile Asn Tyr Asn Ser Leu Ser Val Phe His Ser Ser
 65 70 75 80

Tyr Tyr Arg Leu Pro Asp Phe Asp Ile Pro Ile Val Thr Thr Val His
 85 90 95

Asp Phe Thr Tyr Glu Lys Phe Val Asn Gly Pro Ala Lys Trp Val His
 100 105 110

Ser Trp Gln Lys Asn Arg Ala Val Asn Asn Ser Asp Leu Ile Ile Cys
 115 120 125

Val Ser Glu Asn Thr Ala Lys Asp Leu Gln Met Tyr Cys Ser Val Pro
 130 135 140

Ser Asn Lys Ile Arg Val Ile Tyr Asn Gly Val Ser Asp Lys Tyr His
 145 150 155 160
 Tyr Ile Lys Gly Val Lys Ile Thr Thr Asn Lys Val Ile Phe Val Gly
 165 170 175
 Ala Arg Gly Gly Tyr Lys Asn Phe Asp Ile Ala Val Lys Ala Ile Ser
 180 185 190
 Lys Thr Pro His Leu Glu Leu Ser Val Val Gly Gly Gly Ala Phe Thr
 195 200 205
 Ser Lys Glu Leu Ser Leu Leu Asn His Tyr Leu Pro Gly Arg Tyr His
 210 215 220
 Gly Leu Gly Arg Leu Ser Asp Glu Ala Leu Asn Glu Ala Tyr Asn Ser
 225 230 235 240
 Ala Tyr Ala Leu Leu Tyr Pro Ser Ser Tyr Glu Gly Phe Gly Ile Pro
 245 250 255
 Ile Leu Glu Ala Met Ser Ala Gly Cys Pro Val Ile Ser Val Asn Val
 260 265 270
 Ser Ser Ile Pro Glu Val Ala Gly Asp Ala Ala Ile Leu Val Gln Lys
 275 280 285
 Pro Thr Ile Asp Glu Leu Val Asp Gly Leu Leu Ala Val Glu Ser Glu
 290 295 300
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 305 310 315 320
 Trp Asp Lys Cys Tyr Gln Glu Thr Leu Asp Val Tyr Lys Glu Leu Asn
 325 330 335

Lys

<210> 33
 <211> 990
 <212> DNA
 <213> Yersinia pestis

<220>
 <221> CDS
 <222> (1)..(990)

<400> 33

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gat gga aca tct aca ata tta gat gcg gct ctg gat agt aat ata cat 96
Asp Gly Thr Ser Thr Ile Leu Asp Ala Ala Leu Asp Ser Asn Ile His
20 25 30

att gaa tac agc tgc aaa gat gga acc tgt ggt tct tgt aag gca ata 144
Ile Glu Tyr Ser Cys Lys Asp Gly Thr Cys Gly Ser Cys Lys Ala Ile
35 40 45

ttg att tct ggt gaa gta gac agt gcg gaa aat acc ttt tta act gag 192
Leu Ile Ser Gly Glu Val Asp Ser Ala Glu Asn Thr Phe Leu Thr Glu
50 55 60

gaa gat gtt gct aaa ggt gca atc ctc act tgt tgc tct aag gct aaa 240
Glu Asp Val Ala Lys Gly Ala Ile Leu Thr Cys Cys Ser Lys Ala Lys
65 70 75 80

tct gat att gag tta gat gtt aat tat tat cca gag tta agt cat ata 288
Ser Asp Ile Glu Leu Asp Val Asn Tyr Tyr Pro Glu Leu Ser His Ile
85 90 95

caa aaa aaa act tat cca tgt aaa tta gat agc att gaa ttt att ggt 336
Gln Lys Lys Thr Tyr Pro Cys Lys Leu Asp Ser Ile Glu Phe Ile Gly
100 105 110

gaa gat att gcc att ctc tcc tta cgt ttg cca cca acg gcc aaa ata 384
Glu Asp Ile Ala Ile Leu Ser Leu Arg Leu Pro Pro Thr Ala Lys Ile
115 120 125

cag tat ctg gcg ggc caa tac att gat tta att att aat gga cag cgc 432
Gln Tyr Leu Ala Gly Gln Tyr Ile Asp Leu Ile Ile Asn Gly Gln Arg
130 135 140

cgt agt tac tct att gct aat gct cca ggt ggt aat ggc aat atc gaa 480
Arg Ser Tyr Ser Ile Ala Asn Ala Pro Gly Gly Asn Gly Asn Ile Glu
145 150 155 160

tta cac gta cgt aaa gtt gtt aat ggt gta ttc agc aac atc att ttt 528
Leu His Val Arg Lys Val Val Asn Gly Val Phe Ser Asn Ile Ile Phe
165 170 175

aat gag tta aaa tta cag caa ctt tta cga att gaa ggt cct caa ggg 576
Asn Glu Leu Lys Leu Gln Gln Leu Leu Arg Ile Glu Gly Pro Gln Gly

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180	185	190	
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Thr Phe Phe Val Arg Glu Asp Asn Leu Pro Ile Val Phe Leu Ala Gly			
195	200	205	
gga aca ggt ttt gca cca gtg aaa tca atg gtt gag gcg ttg atc aat	672		
Gly Thr Gly Phe Ala Pro Val Lys Ser Met Val Glu Ala Leu Ile Asn			
210	215	220	
aaa aat gac caa cgg cag gtt cat atc tat tgg gga atg oca gca ggg	720		
Lys Asn Asp Gln Arg Gln Val His Ile Tyr Trp Gly Met Pro Ala Gly			
225	230	235	240
cat aat ttc tat tct gac att gcc aat gag tgg gct ata aaa cac cct	768		
His Asn Phe Tyr Ser Asp Ile Ala Asn Glu Trp Ala Ile Lys His Pro			
245	250	255	
aac att cat tat gtg cct gtt gta tca ggc gat gat agt act tgg acc	816		
Asn Ile His Tyr Val Pro Val Val Ser Gly Asp Asp Ser Thr Trp Thr			
260	265	270	
gga gcc act ggt ttt gta cat caa gcg gtg ctt gaa gat ata ccc gat	864		
Gly Ala Thr Gly Phe Val His Gln Ala Val Leu Glu Asp Ile Pro Asp			
275	280	285	
ctc agc tta ttt aat gtt tat gcc tgt ggt tca tta gcg atg att act	912		
Leu Ser Leu Phe Asn Val Tyr Ala Cys Gly Ser Leu Ala Met Ile Thr			
290	295	300	
gct gct cgt aat gat ttc atc aat cat gga tta gct gaa aat aaa ttt	960		
Ala Ala Arg Asn Asp Phe Ile Asn His Gly Leu Ala Glu Asn Lys Phe			
305	310	315	320
ttc tct gat gcc ttt gtg cca tca aaa taa	990		
Phe Ser Asp Ala Phe Val Pro Ser Lys			
325	330		

<210> 34

<211> 329

<212> PRT

<213> Yersinia pestis

<400> 34

Met Ser Leu Asn Val Lys Leu His Pro Ser Gly Ile Ile Phe Thr Ser

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10

15

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 Ile Glu Tyr Ser Cys Lys Asp Gly Thr Cys Gly Ser Cys Lys Ala Ile
 35 40 45
 Leu Ile Ser Gly Glu Val Asp Ser Ala Glu Asn Thr Phe Leu Thr Glu
 50 55 60
 Glu Asp Val Ala Lys Gly Ala Ile Leu Thr Cys Cys Ser Lys Ala Lys
 65 70 75 80
 Ser Asp Ile Glu Leu Asp Val Asn Tyr Tyr Pro Glu Leu Ser His Ile
 85 90 95
 Gln Lys Lys Thr Tyr Pro Cys Lys Leu Asp Ser Ile Glu Phe Ile Gly
 100 105 110
 Glu Asp Ile Ala Ile Leu Ser Leu Arg Leu Pro Pro Thr Ala Lys Ile
 115 120 125
 Gln Tyr Leu Ala Gly Gln Tyr Ile Asp Leu Ile Ile Asn Gly Gln Arg
 130 135 140
 Arg Ser Tyr Ser Ile Ala Asn Ala Pro Gly Gly Asn Gly Asn Ile Glu
 145 150 155 160
 Leu His Val Arg Lys Val Val Asn Gly Val Phe Ser Asn Ile Ile Phe
 165 170 175
 Asn Glu Leu Lys Leu Gln Gln Leu Leu Arg Ile Glu Gly Pro Gln Gly
 180 185 190
 Thr Phe Phe Val Arg Glu Asp Asn Leu Pro Ile Val Phe Leu Ala Gly
 195 200 205
 Gly Thr Gly Phe Ala Pro Val Lys Ser Met Val Glu Ala Leu Ile Asn
 210 215 220
 Lys Asn Asp Gln Arg Gln Val His Ile Tyr Trp Gly Met Pro Ala Gly
 225 230 235 240
 His Asn Phe Tyr Ser Asp Ile Ala Asn Glu Trp Ala Ile Lys His Pro
 245 250 255
 Asn Ile His Tyr Val Pro Val Val Ser Gly Asp Asp Ser Thr Trp Thr
 260 265 270

Gly Ala Thr Gly Phe Val His Gln Ala Val Leu Glu Asp Ile Pro Asp
 275 280 285

Leu Ser Leu Phe Asn Val Tyr Ala Cys Gly Ser Leu Ala Met Ile Thr
 290 295 300

Ala Ala Arg Asn Asp Phe Ile Asn His Gly Leu Ala Glu Asn Lys Phe
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Phe Ser Asp Ala Phe Val Pro Ser Lys
 325

<210> 35

<211> 3583

<212> DNA

<213> Yersinia pestis

<400> 35

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gttatagtgg atgatatcag tacaaaacag atgtccacca atatgttatt ggtttggatt 180
ggcgtgatgc tcgcgactgc cgtgggtggc tatttgttgc gttatgtctg gcgagtctta 240
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acactgttat cgctattacc gatgccatc atggcgatag tgattaagta ttacggtgac 540
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caagagagcc tgaccagtat tcgcatgatt aaggcctttg gtctggaaga tcgtcagtc 660
caacagtttg ctcaggtagc ggcagaaacc ggtgcgaaga atatgtatgt cgcccgcat 720
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tattcagcgg gcattacagg tgattcgaaa aaataccacg ctggtgggtta ttgctcatcg 3360
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gcagttagtc agcgaagatt tggtgccat tgatcaggaa gctattgata aaggctctat 3540
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<210> 36

<211> 624

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1) .. (624)

<400> 36

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Met Phe Lys Arg Leu Phe Met Val Ala Leu Leu Ala Ile Ala Pro Leu

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1

5

10

15

gtt cat gct gtc gat caa agc aac cct tat cgt ctg atg gat gag gca 96
 Val His Ala Val Asp Gln Ser Asn Pro Tyr Arg Leu Met Asp Glu Ala
 20 25 30

gcg aag aaa acc ttt acg cgt ctg aaa aat gag cag cct aag att aag 144
 Ala Lys Lys Thr Phe Thr Arg Leu Lys Asn Glu Gln Pro Lys Ile Lys
 35 40 45

caa aat cca gat tat ctc cgc acc att gta cgc gaa gag ctg ttg ccg 192
 Gln Asn Pro Asp Tyr Leu Arg Thr Ile Val Arg Glu Glu Leu Leu Pro
 50 55 60

ttt gtt cag atc aaa tac gcc ggc gcg tta gta ctg ggt agc tat tat 240
 Phe Val Gln Ile Lys Tyr Ala Gly Ala Leu Val Leu Gly Ser Tyr Tyr
 65 70 75 80

aaa gat gct aca cct gca cag cgt gaa gcg tat ttc aat gca ttc ggt 288
 Lys Asp Ala Thr Pro Ala Gln Arg Glu Ala Tyr Phe Asn Ala Phe Gly
 85 90 95

aaa tat ctg gag cag gca tac ggg cag gca ttg gcg ttg tat cac ggc 336
 Lys Tyr Leu Glu Gln Ala Tyr Gly Gln Ala Leu Ala Leu Tyr His Gly
 100 105 110

caa act tac gat gtg gca cca gac cag cct tta ggg gat gcc aac atc 384
 Gln Thr Tyr Asp Val Ala Pro Asp Gln Pro Leu Gly Asp Ala Asn Ile
 115 120 125

gtt gct atc cgc gtc acc att ctc gat cca agt ggg cgt cca cct gtc 432
 Val Ala Ile Arg Val Thr Ile Leu Asp Pro Ser Gly Arg Pro Pro Val
 130 135 140

cgg tta gat ttc caa tgg cgt aaa aat agc caa acc ggt aac tgg cag 480
 Arg Leu Asp Phe Gln Trp Arg Lys Asn Ser Gln Thr Gly Asn Trp Gln
 145 150 155 160

gct tat gac atg atc gcc gaa ggg gtg agc atg att agc acc aaa cag 528
 Ala Tyr Asp Met Ile Ala Glu Gly Val Ser Met Ile Ser Thr Lys Gln
 165 170 175

aat gaa tgg gcc tct atc ctg cgc caa aag ggt gtg gat ggt ttg acc 576
 Asn Glu Trp Ala Ser Ile Leu Arg Gln Lys Gly Val Asp Gly Leu Thr
 180 185 190

caa caa ttg ctg agt gcg gct aaa cag cca atc acc tta gat aaa tag 624
 Gln Gln Leu Leu Ser Ala Ala Lys Gln Pro Ile Thr Leu Asp Lys
 195 200 205

<210> 37

<211> 207

<212> PRT

<213> *Yersinia pestis*

<400> 37

Met Phe Lys Arg Leu Phe Met Val Ala Leu Leu Ala Ile Ala Pro Leu
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Val His Ala Val Asp Gln Ser Asn Pro Tyr Arg Leu Met Asp Glu Ala
 20 25 30

Ala Lys Lys Thr Phe Thr Arg Leu Lys Asn Glu Gln Pro Lys Ile Lys
 35 40 45

Gln Asn Pro Asp Tyr Leu Arg Thr Ile Val Arg Glu Glu Leu Leu Pro
 50 55 60

Phe Val Gln Ile Lys Tyr Ala Gly Ala Leu Val Leu Gly Ser Tyr Tyr
 65 70 75 80

Lys Asp Ala Thr Pro Ala Gln Arg Glu Ala Tyr Phe Asn Ala Phe Gly
 85 90 95

Lys Tyr Leu Glu Gln Ala Tyr Gly Gln Ala Leu Ala Leu Tyr His Gly
 100 105 110

Gln Thr Tyr Asp Val Ala Pro Asp Gln Pro Leu Gly Asp Ala Asn Ile
 115 120 125

Val Ala Ile Arg Val Thr Ile Leu Asp Pro Ser Gly Arg Pro Pro Val
 130 135 140

Arg Leu Asp Phe Gln Trp Arg Lys Asn Ser Gln Thr Gly Asn Trp Gln
 145 150 155 160

Ala Tyr Asp Met Ile Ala Glu Gly Val Ser Met Ile Ser Thr Lys Gln
 165 170 175

Asn Glu Trp Ala Ser Ile Leu Arg Gln Lys Gly Val Asp Gly Leu Thr
 180 185 190

Gln Gln Leu Leu Ser Ala Ala Lys Gln Pro Ile Thr Leu Asp Lys
 195 200 205

<210> 38
 <211> 1455
 <212> DNA
 <213> *Yersinia pestis*

<220>
 <221> CDS
 <222> (1)..(1455)

<400> 38
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 Met Gln Thr Asp Val Val Leu Pro Leu Val Gly Tyr Leu Val Leu Val
 1 5 10 15
 ttt ggc tta tct att tat gct tat acg cgc cgc caa acc ggg aat ttt 96
 Phe Gly Leu Ser Ile Tyr Ala Tyr Thr Arg Arg Gln Thr Gly Asn Phe
 20 25 30
 ctc aac gaa tat ttt atc ggc aac cgt tcg atg ggc ggt ttt gta ttg 144
 Leu Asn Glu Tyr Phe Ile Gly Asn Arg Ser Met Gly Gly Phe Val Leu
 35 40 45
 gcg atg acc ctg acc gcc acc tat atc agc gcc agc tcg ttt att ggt 192
 Ala Met Thr Leu Thr Ala Thr Tyr Ile Ser Ala Ser Ser Phe Ile Gly
 50 55 60
 gga cca ggt gcc gct tat aaa tac ggc ctt ggc tgg gtc tta ctg gcg 240
 Gly Pro Gly Ala Ala Tyr Lys Tyr Gly Leu Gly Trp Val Leu Leu Ala
 65 70 75 80
 atg atc caa ttg cct gcg gtc tgg ctt tcc ctc ggt gtc tta ggc aaa 288
 Met Ile Gln Leu Pro Ala Val Trp Leu Ser Leu Gly Val Leu Gly Lys
 85 90 95
 aag ttt gcc att ctg gcg cgt cgc tat aat gcc gtg acc ctc aac gat 336
 Lys Phe Ala Ile Leu Ala Arg Arg Tyr Asn Ala Val Thr Leu Asn Asp
 100 105 110
 atg ttg tat gcc cgt tat cag agc cgt tta ctg gtt tgg ctg gcc agt 384
 Met Leu Tyr Ala Arg Tyr Gln Ser Arg Leu Leu Val Trp Leu Ala Ser
 115 120 125
 atc agc ctg ctg gtg gct ttt gtc ggt gcc atg acc gtg caa ttt att 432
 Ile Ser Leu Leu Val Ala Phe Val Gly Ala Met Thr Val Gln Phe Ile
 130 135 140
 ggt ggc gca cgg ttg tta gaa acg gcg gcg ggg atc cct tac gac act 480
 Gly Gly Ala Arg Leu Leu Glu Thr Ala Ala Gly Ile Pro Tyr Asp Thr

145	150	155	160	
ggc tta ttg att ttt ggt atc agt atc gcc ctg tae acc tcg ttt ggt				528
Gly Leu Leu Ile Phe Gly Ile Ser Ile Ala Leu Tyr Thr Ser Phe Gly				
	165	170	175	
ggc ttc cgg gcc agt gtc ttg aat gat gcc ctg caa ggg tta gtg atg				576
Gly Phe Arg Ala Ser Val Leu Asn Asp Ala Leu Gln Gly Leu Val Met				
	180	185	190	
ctg atc ggc acc att tta ctg tta gtt gcg gtg atc cac gcg gca ggt				624
Leu Ile Gly Thr Ile Leu Leu Leu Val Ala Val Ile His Ala Ala Gly				
	195	200	205	
ggc cta cac aaa gcc gtc gaa acg ctg caa cat atc gat ccg gcg ctg				672
Gly Leu His Lys Ala Val Glu Thr Leu Gln His Ile Asp Pro Ala Leu				
	210	215	220	
gtt tcc ccc caa ggc ggc gat cag atc ctc gac gtg cca ttt atg gct				720
Val Ser Pro Gln Gly Gly Asp Gln Ile Leu Asp Val Pro Phe Met Ala				
	225	230	235	240
tcg ttc tgg atc ctg gtc tgt ttt ggg gtg att ggt ctg cca cac acc				768
Ser Phe Trp Ile Leu Val Cys Phe Gly Val Ile Gly Leu Pro His Thr				
	245	250	255	
gcc gta cgt tgt att tcg tat cgt gac agt aaa gcg gtt cat cgc ggt				816
Ala Val Arg Cys Ile Ser Tyr Arg Asp Ser Lys Ala Val His Arg Gly				
	260	265	270	
att atc ctc ggc acc atc gtg gtg gcg atc cta atg ttc ggt atg cac				864
Ile Ile Leu Gly Thr Ile Val Val Ala Ile Leu Met Phe Gly Met His				
	275	280	285	
ctg gct ggc gca ctg ggg cgg gcg gtg tta cca gat ctg aaa att cca				912
Leu Ala Gly Ala Leu Gly Arg Ala Val Leu Pro Asp Leu Lys Ile Pro				
	290	295	300	
gat caa gta atc ccg aca ctg atg atc acc gta ctg ccg cca ttt gct				960
Asp Gln Val Ile Pro Thr Leu Met Ile Thr Val Leu Pro Pro Phe Ala				
	305	310	315	320
gcg ggg ata ttc ctg gca gca ccg atg gcg gcg atc atg tcg acc atc				1008
Ala Gly Ile Phe Leu Ala Ala Pro Met Ala Ala Ile Met Ser Thr Ile				
	325	330	335	
aat gcc cag tta ctg caa tct tct gct acc atc gtg aag gat ttg tat				1056
Asn Ala Gln Leu Leu Gln Ser Ser Ala Thr Ile Val Lys Asp Leu Tyr				

340	345	350	
ctc aat ctg tgg cca gca gag tta aag aat gag cgc aag ctg gca cgt			1104
Leu Asn Leu Trp Pro Ala Glu Leu Lys Asn Glu Arg Lys Leu Ala Arg			
355	360	365	
atc tcc agc tta tcc aca ctc att ctt ggg cta tta ttg ctc ttg gcc			1152
Ile Ser Ser Leu Ser Thr Leu Ile Leu Gly Leu Leu Leu Leu Ala			
370	375	380	
gcc tgg cga cca cct gaa atg att atc tgg ttg aac cta ctg gcc ttt			1200
Ala Trp Arg Pro Pro Glu Met Ile Ile Trp Leu Asn Leu Leu Ala Phe			
385	390	395	400
ggc gga ctg gaa gcg gta ttc ctc tgg cca ttg gta ttg gga tta tac			1248
Gly Gly Leu Glu Ala Val Phe Leu Trp Pro Leu Val Leu Gly Leu Tyr			
405	410	415	
tgg gag cga gcc aat gcc cac ggc gct ctt agc gcc atg atc gtc ggt			1296
Trp Glu Arg Ala Asn Ala His Gly Ala Leu Ser Ala Met Ile Val Gly			
420	425	430	
gcg gta tgc tat acg gta tta gcc agc ttc gac atc aag ata gcc ggc			1344
Ala Val Cys Tyr Thr Val Leu Ala Ser Phe Asp Ile Lys Ile Ala Gly			
435	440	445	
ctg cac ccc att gtg ccg tca ctt aca ctt aat ctg ttg gcg ttt tat			1392
Leu His Pro Ile Val Pro Ser Leu Thr Leu Asn Leu Leu Ala Phe Tyr			
450	455	460	
atc ggt aat ctg ttt ggc gac aga gcg cgg gcg cga cac ccc gcc atc			1440
Ile Gly Asn Leu Phe Gly Asp Arg Ala Arg Ala Arg His Pro Ala Ile			
465	470	475	480
gtc agt gcc gat taa			1455
Val Ser Ala Asp			
485			

<210> 39

<211> 484

<212> PRT

<213> Yersinia pestis

<400> 39

Met Gln Thr Asp Val Val Leu Pro Leu Val Gly Tyr Leu Val Leu Val

1

5

10

15

Phe Gly Leu Ser Ile Tyr Ala Tyr Thr Arg Arg Gln Thr Gly Asn Phe
 20 25 30

Leu Asn Glu Tyr Phe Ile Gly Asn Arg Ser Met Gly Gly Phe Val Leu
 35 40 45

Ala Met Thr Leu Thr Ala Thr Tyr Ile Ser Ala Ser Ser Phe Ile Gly
 50 55 60

Gly Pro Gly Ala Ala Tyr Lys Tyr Gly Leu Gly Trp Val Leu Leu Ala
 65 70 75 80

Met Ile Gln Leu Pro Ala Val Trp Leu Ser Leu Gly Val Leu Gly Lys
 85 90 95

Lys Phe Ala Ile Leu Ala Arg Arg Tyr Asn Ala Val Thr Leu Asn Asp
 100 105 110

Met Leu Tyr Ala Arg Tyr Gln Ser Arg Leu Leu Val Trp Leu Ala Ser
 115 120 125

Ile Ser Leu Leu Val Ala Phe Val Gly Ala Met Thr Val Gln Phe Ile
 130 135 140

Gly Gly Ala Arg Leu Leu Glu Thr Ala Ala Gly Ile Pro Tyr Asp Thr
 145 150 155 160

Gly Leu Leu Ile Phe Gly Ile Ser Ile Ala Leu Tyr Thr Ser Phe Gly
 165 170 175

Gly Phe Arg Ala Ser Val Leu Asn Asp Ala Leu Gln Gly Leu Val Met
 180 185 190

Leu Ile Gly Thr Ile Leu Leu Leu Val Ala Val Ile His Ala Ala Gly
 195 200 205

Gly Leu His Lys Ala Val Glu Thr Leu Gln His Ile Asp Pro Ala Leu
 210 215 220

Val Ser Pro Gln Gly Gly Asp Gln Ile Leu Asp Val Pro Phe Met Ala
 225 230 235 240

Ser Phe Trp Ile Leu Val Cys Phe Gly Val Ile Gly Leu Pro His Thr
 245 250 255

Ala Val Arg Cys Ile Ser Tyr Arg Asp Ser Lys Ala Val His Arg Gly
 260 265 270

Ile Ile Leu Gly Thr Ile Val Val Ala Ile Leu Met Phe Gly Met His
 275 280 285

Leu Ala Gly Ala Leu Gly Arg Ala Val Leu Pro Asp Leu Lys Ile Pro
 290 295 300

Asp Gln Val Ile Pro Thr Leu Met Ile Thr Val Leu Pro Pro Phe Ala
 305 310 315 320

Ala Gly Ile Phe Leu Ala Ala Pro Met Ala Ala Ile Met Ser Thr Ile
 325 330 335

Asn Ala Gln Leu Leu Gln Ser Ser Ala Thr Ile Val Lys Asp Leu Tyr
 340 345 350

Leu Asn Leu Trp Pro Ala Glu Leu Lys Asn Glu Arg Lys Leu Ala Arg
 355 360 365

Ile Ser Ser Leu Ser Thr Leu Ile Leu Gly Leu Leu Leu Leu Ala
 370 375 380

Ala Trp Arg Pro Pro Glu Met Ile Ile Trp Leu Asn Leu Leu Ala Phe
 385 390 395 400

Gly Gly Leu Glu Ala Val Phe Leu Trp Pro Leu Val Leu Gly Leu Tyr
 405 410 415

Trp Glu Arg Ala Asn Ala His Gly Ala Leu Ser Ala Met Ile Val Gly
 420 425 430

Ala Val Cys Tyr Thr Val Leu Ala Ser Phe Asp Ile Lys Ile Ala Gly
 435 440 445

Leu His Pro Ile Val Pro Ser Leu Thr Leu Asn Leu Leu Ala Phe Tyr
 450 455 460

Ile Gly Asn Leu Phe Gly Asp Arg Ala Arg Ala Arg His Pro Ala Ile
 465 470 475 480

Val Ser Ala Asp

<210> 40

<211> 879

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(879)

<400> 40

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atg gcg aga ttt tgg cag ata ctg att gcg tta tta ctg gtg cca aca 48
Met Ala Arg Phe Trp Gln Ile Leu Ile Ala Leu Leu Leu Val Pro Thr
  1           5           10          15

ttg gca cag gct gaa gaa gca acg att gaa aag att cat gat gcg ccc 96
Leu Ala Gln Ala Glu Glu Ala Thr Ile Glu Lys Ile His Asp Ala Pro
      20           25           30

gca gtg cgt ggc agt att atc gcg gca atg ttg cag gac cac gat aat 144
Ala Val Arg Gly Ser Ile Ile Ala Ala Met Leu Gln Asp His Asp Asn
      35           40           45

cct ttc cta ctt tat ccg tat gaa acc aac tat ttg ctc tac acc tat 192
Pro Phe Leu Leu Tyr Pro Tyr Glu Thr Asn Tyr Leu Leu Tyr Thr Tyr
      50           55           60

acc aac gag atc aat aaa caa gcc att agc tcg tat gat tgg gct gaa 240
Thr Asn Glu Ile Asn Lys Gln Ala Ile Ser Ser Tyr Asp Trp Ala Glu
      65           70           75           80

cag gcg aat aaa gat gaa gta aaa ttc caa ctg agt tta gct ttc cct 288
Gln Ala Asn Lys Asp Glu Val Lys Phe Gln Leu Ser Leu Ala Phe Pro
      85           90           95

atc tgg cgt ggt att gcc ggg gat aac tca tta ttg ggg gct tct tat 336
Ile Trp Arg Gly Ile Ala Gly Asp Asn Ser Leu Leu Gly Ala Ser Tyr
      100          105          110

acc cag cgt tca tgg tgg cag gca tcc aac agt gaa gaa tct tca cct 384
Thr Gln Arg Ser Trp Trp Gln Ala Ser Asn Ser Glu Glu Ser Ser Pro
      115          120          125

ttt cgt gaa acc aac tac gag cca cag ctg ttt ttg gcg tgg tca aca 432
Phe Arg Glu Thr Asn Tyr Glu Pro Gln Leu Phe Leu Ala Trp Ser Thr
      130          135          140

gat tac gaa ttg gct ggc tgg act ttc cgc gaa gtc gaa ttt ggt ttt 480
Asp Tyr Glu Leu Ala Gly Trp Thr Phe Arg Glu Val Glu Phe Gly Phe
      145          150          155          160

aac cat caa tcc aac ggt aaa gct gac cca acc tca cgt agt tgg aac 528
Asn His Gln Ser Asn Gly Lys Ala Asp Pro Thr Ser Arg Ser Trp Asn
      165          170          175

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cgt gtt tat acc cgc gtg atg gca caa cgt ggc aat ttg gaa atc gac 576
 Arg Val Tyr Thr Arg Val Met Ala Gln Arg Gly Asn Leu Glu Ile Asp
 180 185 190

ctg aag cct tgg tat cgt att cct gaa agc gac agt aaa gat gat aac 624
 Leu Lys Pro Trp Tyr Arg Ile Pro Glu Ser Asp Ser Lys Asp Asp Asn
 195 200 205

cct gat att acg aaa tac atg ggg tat tat cgc ctg aaa gtc ggc tat 672
 Pro Asp Ile Thr Lys Tyr Met Gly Tyr Tyr Arg Leu Lys Val Gly Tyr
 210 215 220

gcc ctg ggt gac agc gta ttc agc ctt gat ggt cgc tat aac tgg aat 720
 Ala Leu Gly Asp Ser Val Phe Ser Leu Asp Gly Arg Tyr Asn Trp Asn
 225 230 235 240

acc ggt tac ggt ggc gcg gaa atg ggc tgg agc tac cca att acc aaa 768
 Thr Gly Tyr Gly Gly Ala Glu Met Gly Trp Ser Tyr Pro Ile Thr Lys
 245 250 255

cat gtt cgc ttc tat act cag gta ttc agt ggc tac ggt gag tca atg 816
 His Val Arg Phe Tyr Thr Gln Val Phe Ser Gly Tyr Gly Glu Ser Met
 260 265 270

att gac tat aac ttt agg caa aca cgg gtg ggt gta ggt atc atg ttg 864
 Ile Asp Tyr Asn Phe Arg Gln Thr Arg Val Gly Val Gly Ile Met Leu
 275 280 285

aac gat gtc ctt taa 879
 Asn Asp Val Leu
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<210> 41

<211> 292

<212> PRT

<213> *Yersinia pestis*

<400> 41

Met Ala Arg Phe Trp Gln Ile Leu Ile Ala Leu Leu Leu Val Pro Thr
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Leu Ala Gln Ala Glu Glu Ala Thr Ile Glu Lys Ile His Asp Ala Pro
 20 25 30

Ala Val Arg Gly Ser Ile Ile Ala Ala Met Leu Gln Asp His Asp Asn
 35 40 45

Pro Phe Leu Leu Tyr Pro Tyr Glu Thr Asn Tyr Leu Leu Tyr Thr Tyr
 50 55 60

Thr Asn Glu Ile Asn Lys Gln Ala Ile Ser Ser Tyr Asp Trp Ala Glu
 65 70 75 80

Gln Ala Asn Lys Asp Glu Val Lys Phe Gln Leu Ser Leu Ala Phe Pro
 85 90 95

Ile Trp Arg Gly Ile Ala Gly Asp Asn Ser Leu Leu Gly Ala Ser Tyr
 100 105 110

Thr Gln Arg Ser Trp Trp Gln Ala Ser Asn Ser Glu Glu Ser Ser Pro
 115 120 125

Phe Arg Glu Thr Asn Tyr Glu Pro Gln Leu Phe Leu Ala Trp Ser Thr
 130 135 140

Asp Tyr Glu Leu Ala Gly Trp Thr Phe Arg Glu Val Glu Phe Gly Phe
 145 150 155 160

Asn His Gln Ser Asn Gly Lys Ala Asp Pro Thr Ser Arg Ser Trp Asn
 165 170 175

Arg Val Tyr Thr Arg Val Met Ala Gln Arg Gly Asn Leu Glu Ile Asp
 180 185 190

Leu Lys Pro Trp Tyr Arg Ile Pro Glu Ser Asp Ser Lys Asp Asp Asn
 195 200 205

Pro Asp Ile Thr Lys Tyr Met Gly Tyr Tyr Arg Leu Lys Val Gly Tyr
 210 215 220

Ala Leu Gly Asp Ser Val Phe Ser Leu Asp Gly Arg Tyr Asn Trp Asn
 225 230 235 240

Thr Gly Tyr Gly Gly Ala Glu Met Gly Trp Ser Tyr Pro Ile Thr Lys
 245 250 255

His Val Arg Phe Tyr Thr Gln Val Phe Ser Gly Tyr Gly Glu Ser Met
 260 265 270

Ile Asp Tyr Asn Phe Arg Gln Thr Arg Val Gly Val Gly Ile Met Leu
 275 280 285

Asn Asp Val Leu
 290

<210> 42
 <211> 2556
 <212> DNA
 <213> *Yersinia pestis*

<220>
 <221> CDS
 <222> (1)..(2556)

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 ttg ttc ttc aac ttg ctc gtg gtg gcg gtc acc ctg atg gtg agt ggt 96
 Leu Phe Phe Asn Leu Leu Val Val Ala Val Thr Leu Met Val Ser Gly
 20 25 30
 gtc gcg gtg ctg ggc ttc gag cag gca agc cgc tta caa aag cag gtc 144
 Val Ala Val Leu Gly Phe Glu Gln Ala Ser Arg Leu Gln Lys Gln Val
 35 40 45
 cag gag cgg aca ctg cgc gat atg tca agc agc atg gcg ctg gcg cgc 192
 Gln Glu Arg Thr Leu Arg Asp Met Ser Ser Ser Met Ala Leu Ala Arg
 50 55 60
 gat acc gca aat gtg gcg acg gcg gcg gtg cgg ctt tcc caa gtg gtt 240
 Asp Thr Ala Asn Val Ala Thr Ala Ala Val Arg Leu Ser Gln Val Val
 65 70 75 80
 ggg gcg ctt gaa ttc cag agt gaa gcg gcc agt ctt caa gag acg caa 288
 Gly Ala Leu Glu Phe Gln Ser Glu Ala Ala Ser Leu Gln Glu Thr Gln
 85 90 95
 ctg gcg tta cga agt tca ctc gct cat ctt gct aat gcc ccg ctt gcc 336
 Leu Ala Leu Arg Ser Ser Leu Ala His Leu Ala Asn Ala Pro Leu Ala
 100 105 110
 agc cat gaa ccg cta ttg gtg aaa cgt atc att gag cgt agc aat gaa 384
 Ser His Glu Pro Leu Leu Val Lys Arg Ile Ile Glu Arg Ser Asn Glu
 115 120 125
 ctg gaa acc agc gtt gca cgt atg ctg aat ttg ggt cac cgt cgc cat 432
 Leu Glu Thr Ser Val Ala Arg Met Leu Asn Leu Gly His Arg Arg His
 130 135 140

ctt gag cgt aac ctg ctg ctg agc gcc ctc tat cag acc caa agt tat 480
 Leu Glu Arg Asn Leu Leu Leu Ser Ala Leu Tyr Gln Thr Gln Ser Tyr
 145 150 155 160

ctt cac cat ctg cag gag att aac cag cgc gat ggg ctg aac aaa ccc 528
 Leu His His Leu Gln Glu Ile Asn Gln Arg Asp Gly Leu Asn Lys Pro
 165 170 175

gat gcc gca ctg cta aaa gag atg gat cgc ctg cta ctg gtg gct atc 576
 Asp Ala Ala Leu Leu Lys Glu Met Asp Arg Leu Leu Leu Val Ala Ile
 180 185 190

cag acc tcc tcg ccc aaa gct gcc gta cag caa ctt act gag gtg atg 624
 Gln Thr Ser Ser Pro Lys Ala Ala Val Gln Gln Leu Thr Glu Val Met
 195 200 205

cag gca ttg cct gcc cat gct gac tcg ccg ctg gtg gag gaa atc ttg 672
 Gln Ala Leu Pro Ala His Ala Asp Ser Pro Leu Val Glu Glu Ile Leu
 210 215 220

caa gag ttc agc gcc agc ctg tat cag ctg ctg ccg ttg tcc atc acg 720
 Gln Glu Phe Ser Ala Ser Leu Tyr Gln Leu Leu Pro Leu Ser Ile Thr
 225 230 235 240

ctt gaa aat agc gat ctg agc att acc tgg tac atg tac cac gtc aaa 768
 Leu Glu Asn Ser Asp Leu Ser Ile Thr Trp Tyr Met Tyr His Val Lys
 245 250 255

gcg ttg gtg gcg ttt ctc aat cag ggc atc aat atc tat gta caa aag 816
 Ala Leu Val Ala Phe Leu Asn Gln Gly Ile Asn Ile Tyr Val Gln Lys
 260 265 270

gtg ggg gag gaa tcg ctg cag cgt agc caa caa aac cac aaa gcc ttg 864
 Val Gly Glu Glu Ser Leu Gln Arg Ser Gln Gln Asn His Lys Ala Leu
 275 280 285

caa tcg atc atc acg tct att ggt ctg ttt gcc ctg ttg gca ctg gtt 912
 Gln Ser Ile Ile Thr Ser Ile Gly Leu Phe Ala Leu Leu Ala Leu Val
 290 295 300

atc acc ggg ttt gcc ggc tgg tat atc tac cat aac ctt ggc tct aac 960
 Ile Thr Gly Phe Ala Gly Trp Tyr Ile Tyr His Asn Leu Gly Ser Asn
 305 310 315 320

tta acg gcg ata tct cat gcc atg acc cga ttg gca aga gga gaa aaa 1008
 Leu Thr Ala Ile Ser His Ala Met Thr Arg Leu Ala Arg Gly Glu Lys
 325 330 335

gag gtc agc gta cca gcc caa caa cgg cgt gat gaa ctg ggc gaa ctg	1056
Glu Val Ser Val Pro Ala Gln Gln Arg Arg Asp Glu Leu Gly Glu Leu	
340 345 350	
gct cgc gcg ttt aac gtt ttt gcc cgc aat acc gct tcg ctg gag cag	1104
Ala Arg Ala Phe Asn Val Phe Ala Arg Asn Thr Ala Ser Leu Glu Gln	
355 360 365	
aca tca cgt ctt ctg aaa gag aaa agt acg cta ttg gaa acc acc ttt	1152
Thr Ser Arg Leu Leu Lys Glu Lys Ser Thr Leu Leu Glu Thr Thr Phe	
370 375 380	
cac gct atg cgc gat ggt ttt gcc ctg ttc gac aac gag ggc ttt ctg	1200
His Ala Met Arg Asp Gly Phe Ala Leu Phe Asp Asn Glu Gly Phe Leu	
385 390 395 400	
gtg gtg tgg aac ccg caa tac cca ctg ttg ctg ggg ctg gca ccg gag	1248
Val Val Trp Asn Pro Gln Tyr Pro Leu Leu Leu Gly Leu Ala Pro Glu	
405 410 415	
cag cta cag cat ggt cag cac tac ctt caa tta ttg aag cag atg acg	1296
Gln Leu Gln His Gly Gln His Tyr Leu Gln Leu Leu Lys Gln Met Thr	
420 425 430	
cca ctg caa gag cat ata ctt gag aac ctc gcc ctc ccg ctg cca aaa	1344
Pro Leu Gln Glu His Ile Leu Glu Asn Leu Ala Leu Pro Leu Pro Lys	
435 440 445	
acc caa gag cta aga ctt gag gac cat cgc act atc gaa ctg cgt ttc	1392
Thr Gln Glu Leu Arg Leu Glu Asp His Arg Thr Ile Glu Leu Arg Phe	
450 455 460	
agt ccg gtt cct gga cga ggg atg gtt aat gtg gtg ttg gat cgt agc	1440
Ser Pro Val Pro Gly Arg Gly Met Val Asn Val Val Leu Asp Arg Ser	
465 470 475 480	
gag cgc aaa gca ctg gaa gaa gcg ctg gtc cat agc caa aaa atg aag	1488
Glu Arg Lys Ala Leu Glu Glu Ala Leu Val His Ser Gln Lys Met Lys	
485 490 495	
gcg gta ggg cag ctc acg ggc ggc ctg gct cat gat ttt aat aac ctg	1536
Ala Val Gly Gln Leu Thr Gly Gly Leu Ala His Asp Phe Asn Asn Leu	
500 505 510	
ctg gcg gtg att att ggc agt ctt gag cta acc gct acg gac tcg tcg	1584
Leu Ala Val Ile Ile Gly Ser Leu Glu Leu Thr Ala Thr Asp Ser Ser	
515 520 525	

gat gcc acg cgt att cat cgt gct ctg aag gcc gct gag cgg ggg gcg	1632
Asp Ala Thr Arg Ile His Arg Ala Leu Lys Ala Ala Glu Arg Gly Ala	
530 535 540	
caa ctc acc caa cgg ttg ctg gcg ttc tca cgc aag cag tcg ctt cac	1680
Gln Leu Thr Gln Arg Leu Leu Ala Phe Ser Arg Lys Gln Ser Leu His	
545 550 555 560	
cct cga gct gtt gcg atg aaa gaa cta ctt gat aac ctg gac ccg ctg	1728
Pro Arg Ala Val Ala Met Lys Glu Leu Leu Asp Asn Leu Asp Pro Leu	
565 570 575	
ata cgc cac tcg ctt ccg gct cat ctt acg ctc aca att gaa gct cag	1776
Ile Arg His Ser Leu Pro Ala His Leu Thr Leu Thr Ile Glu Ala Gln	
580 585 590	
cag cct gcc tgg cac gcc tgg ata gac gta aac caa ctg gaa aac gca	1824
Gln Pro Ala Trp His Ala Trp Ile Asp Val Asn Gln Leu Glu Asn Ala	
595 600 605	
att atc aat ctg gtg atg aat gct cgc gac gcg atg gaa ggg cgc agc	1872
Ile Ile Asn Leu Val Met Asn Ala Arg Asp Ala Met Glu Gly Arg Ser	
610 615 620	
ggc gag att aaa atc cgc acc tgg aat caa cgc gta gag cgt ggt gaa	1920
Gly Glu Ile Lys Ile Arg Thr Trp Asn Gln Arg Val Glu Arg Gly Glu	
625 630 635 640	
ggg cgc aaa caa gat atg gtg gtg ctg gaa gtg gct gat agc ggc cat	1968
Gly Arg Lys Gln Asp Met Val Val Leu Glu Val Ala Asp Ser Gly His	
645 650 655	
ggc atg acc acc gca gtg aaa gag cag gtt ttt gaa ccc ttc ttc acc	2016
Gly Met Thr Thr Ala Val Lys Glu Gln Val Phe Glu Pro Phe Phe Thr	
660 665 670	
acc aag caa acc ggt agc ggg agt ggg ctt ggg ctg tca atg gta tac	2064
Thr Lys Gln Thr Gly Ser Gly Ser Gly Leu Gly Leu Ser Met Val Tyr	
675 680 685	
ggc ttt gtg cgc cag tcc gga ggg cgg gta cag ata gaa agt gaa ccg	2112
Gly Phe Val Arg Gln Ser Gly Gly Arg Val Gln Ile Glu Ser Glu Pro	
690 695 700	
ggg aaa ggg acc cgg gtc tgc ttg cag tta ccc cgt gca ctc aca caa	2160
Gly Lys Gly Thr Arg Val Cys Leu Gln Leu Pro Arg Ala Leu Thr Gln	
705 710 715 720	

agt ctg ata gaa gtc ctg cca gcg ctt ggt gcc gtt gcg aat atg gct 2208
 Ser Leu Ile Glu Val Leu Pro Ala Leu Gly Ala Val Ala Asn Met Ala
 725 730 735

gat cag cta gtc tta gtg ctg gaa gat gag ccg gat gta cgc cag acc 2256
 Asp Gln Leu Val Leu Val Leu Glu Asp Glu Pro Asp Val Arg Gln Thr
 740 745 750

ctg tgc gag caa ctc cat caa ctg ggc tac ctg acg ctt gaa acc ggc 2304
 Leu Cys Glu Gln Leu His Gln Leu Gly Tyr Leu Thr Leu Glu Thr Gly
 755 760 765

gac agt cgg cag gcg ctg gca ttg atg gcc gac gtg ccg gat atc agc 2352
 Asp Ser Arg Gln Ala Leu Ala Leu Met Ala Asp Val Pro Asp Ile Ser
 770 775 780

att gtg ata agc gac tta atg cta ccc ggc gac atg acc ggt gcg gaa 2400
 Ile Val Ile Ser Asp Leu Met Leu Pro Gly Asp Met Thr Gly Ala Glu
 785 790 795 800

gtg ctt cag caa gcg cgc agt gtt tat cct cat ctt aag ctg ttg tta 2448
 Val Leu Gln Gln Ala Arg Ser Val Tyr Pro His Leu Lys Leu Leu Leu
 805 810 815

att agt ggc cag gat ctg cgg cgc agc aag aat ttc atg ccg gag gtg 2496
 Ile Ser Gly Gln Asp Leu Arg Arg Ser Lys Asn Phe Met Pro Glu Val
 820 825 830

gaa ctg ctg cgt aag cct ttt aac caa caa cag cta gta cag gcg ctg 2544
 Glu Leu Leu Arg Lys Pro Phe Asn Gln Gln Gln Leu Val Gln Ala Leu
 835 840 845

caa aga gtc tga 2556
 Gln Arg Val
 850

<210> 43

<211> 851

<212> PRT

<213> Yersinia pestis

<400> 43

Met Glu Gln Pro Arg Leu Ser Phe Phe Ala Ser Val Arg Gly Arg Leu
 1 5 10 15

Leu Phe Phe Asn Leu Leu Val Val Ala Val Thr Leu Met Val Ser Gly

73

275	280	285
Gln Ser Ile Ile Thr Ser Ile Gly Leu Phe Ala Leu Leu Ala Leu Val		
290	295	300
Ile Thr Gly Phe Ala Gly Trp Tyr Ile Tyr His Asn Leu Gly Ser Asn		
305	310	315 320
Leu Thr Ala Ile Ser His Ala Met Thr Arg Leu Ala Arg Gly Glu Lys		
325	330	335
Glu Val Ser Val Pro Ala Gln Gln Arg Arg Asp Glu Leu Gly Glu Leu		
340	345	350
Ala Arg Ala Phe Asn Val Phe Ala Arg Asn Thr Ala Ser Leu Glu Gln		
355	360	365
Thr Ser Arg Leu Leu Lys Glu Lys Ser Thr Leu Leu Glu Thr Thr Phe		
370	375	380
His Ala Met Arg Asp Gly Phe Ala Leu Phe Asp Asn Glu Gly Phe Leu		
385	390	395 400
Val Val Trp Asn Pro Gln Tyr Pro Leu Leu Leu Gly Leu Ala Pro Glu		
405	410	415
Gln Leu Gln His Gly Gln His Tyr Leu Gln Leu Leu Lys Gln Met Thr		
420	425	430
Pro Leu Gln Glu His Ile Leu Glu Asn Leu Ala Leu Pro Leu Pro Lys		
435	440	445
Thr Gln Glu Leu Arg Leu Glu Asp His Arg Thr Ile Glu Leu Arg Phe		
450	455	460
Ser Pro Val Pro Gly Arg Gly Met Val Asn Val Val Leu Asp Arg Ser		
465	470	475 480
Glu Arg Lys Ala Leu Glu Glu Ala Leu Val His Ser Gln Lys Met Lys		
485	490	495
Ala Val Gly Gln Leu Thr Gly Gly Leu Ala His Asp Phe Asn Asn Leu		
500	505	510
Leu Ala Val Ile Ile Gly Ser Leu Glu Leu Thr Ala Thr Asp Ser Ser		
515	520	525
Asp Ala Thr Arg Ile His Arg Ala Leu Lys Ala Ala Glu Arg Gly Ala		

530	535	540
Gln Leu Thr Gln Arg Leu Leu Ala Phe Ser Arg Lys Gln Ser Leu His		
545	550	555 560
Pro Arg Ala Val Ala Met Lys Glu Leu Leu Asp Asn Leu Asp Pro Leu		
565	570	575
Ile Arg His Ser Leu Pro Ala His Leu Thr Leu Thr Ile Glu Ala Gln		
580	585	590
Gln Pro Ala Trp His Ala Trp Ile Asp Val Asn Gln Leu Glu Asn Ala		
595	600	605
Ile Ile Asn Leu Val Met Asn Ala Arg Asp Ala Met Glu Gly Arg Ser		
610	615	620
Gly Glu Ile Lys Ile Arg Thr Trp Asn Gln Arg Val Glu Arg Gly Glu		
625	630	635 640
Gly Arg Lys Gln Asp Met Val Val Leu Glu Val Ala Asp Ser Gly His		
645	650	655
Gly Met Thr Thr Ala Val Lys Glu Gln Val Phe Glu Pro Phe Phe Thr		
660	665	670
Thr Lys Gln Thr Gly Ser Gly Ser Gly Leu Gly Leu Ser Met Val Tyr		
675	680	685
Gly Phe Val Arg Gln Ser Gly Gly Arg Val Gln Ile Glu Ser Glu Pro		
690	695	700
Gly Lys Gly Thr Arg Val Cys Leu Gln Leu Pro Arg Ala Leu Thr Gln		
705	710	715 720
Ser Leu Ile Glu Val Leu Pro Ala Leu Gly Ala Val Ala Asn Met Ala		
725	730	735
Asp Gln Leu Val Leu Val Leu Glu Asp Glu Pro Asp Val Arg Gln Thr		
740	745	750
Leu Cys Glu Gln Leu His Gln Leu Gly Tyr Leu Thr Leu Glu Thr Gly		
755	760	765
Asp Ser Arg Gln Ala Leu Ala Leu Met Ala Asp Val Pro Asp Ile Ser		
770	775	780
Ile Val Ile Ser Asp Leu Met Leu Pro Gly Asp Met Thr Gly Ala Glu		

785	790	795	800
Val Leu Gln Gln Ala Arg Ser Val Tyr Pro His Leu Lys Leu Leu Leu			
	805	810	815
Ile Ser Gly Gln Asp Leu Arg Arg Ser Lys Asn Phe Met Pro Glu Val			
	820	825	830
Glu Leu Leu Arg Lys Pro Phe Asn Gln Gln Gln Leu Val Gln Ala Leu			
	835	840	845
Gln Arg Val			
850			

<210> 44

<211> 1764

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(1764)

<400> 44

atg gac gac tta acc ctg cgt tat ttt gac gct gaa atg cgc tac ctg	48
Met Asp Asp Leu Thr Leu Arg Tyr Phe Asp Ala Glu Met Arg Tyr Leu	
1 5 10 15	

cgc gaa gcg ggc gaa gag ttt gct cgt gcg cac cct gat cgg gct gcc	96
Arg Glu Ala Gly Glu Glu Phe Ala Arg Ala His Pro Asp Arg Ala Ala	
20 25 30	

gga tta aat ctg gat aaa gcc ggg gcg cgt gac ccc tat gtc gaa cgc	144
Gly Leu Asn Leu Asp Lys Ala Gly Ala Arg Asp Pro Tyr Val Glu Arg	
35 40 45	

cta ttt gaa ggc ttt gcc ttt ctg atg ggc cga ctg cgg gaa aaa ctg	192
Leu Phe Glu Gly Phe Ala Phe Leu Met Gly Arg Leu Arg Glu Lys Leu	
50 55 60	

gat gac gac ctg ccg gaa ctg acc gaa ggg ttg gtc agc ctg ctg tgg	240
Asp Asp Asp Leu Pro Glu Leu Thr Glu Gly Leu Val Ser Leu Leu Trp	
65 70 75 80	

ccg cac tac ctg cgt acc att ccg tcg ctt tct att gtg gag ttc acc	288
Pro His Tyr Leu Arg Thr Ile Pro Ser Leu Ser Ile Val Glu Phe Thr	

85	90	95	
cca caa tgg cag ggg atg aaa gag cgc atg ggg gtg agt aaa ggt ttt			336
Pro Gln Trp Gln Gly Met Lys Glu Arg Met Gly Val Ser Lys Gly Phe			
100	105	110	
gaa gtg ctg tcc cgc ccc att ggt gaa cgt gaa acc cgt tgc cgc tat			384
Glu Val Leu Ser Arg Pro Ile Gly Glu Arg Glu Thr Arg Cys Arg Tyr			
115	120	125	
acc acc acg caa gag atg gac ctg ctc ccg ctg acc ctg cgc cgt gcc			432
Thr Thr Thr Gln Glu Met Asp Leu Leu Pro Leu Thr Leu Arg Arg Ala			
130	135	140	
ggg ctg gac agt gaa ccc gat ggc cgg tcg gtt atc cgg ctg cgc ttt			480
Gly Leu Asp Ser Glu Pro Asp Gly Arg Ser Val Ile Arg Leu Arg Phe			
145	150	155	160
gat tgc agc gcg ctg gcc gac tgg agc cgt atc aac ctg agc cgc ctg			528
Asp Cys Ser Ala Leu Ala Asp Trp Ser Arg Ile Asn Leu Ser Arg Leu			
165	170	175	
ccg ctc tat ttt gat gcc gat gcg ccg ctg gcc tgc gcc ctg cat gag			576
Pro Leu Tyr Phe Asp Ala Asp Ala Pro Leu Ala Cys Ala Leu His Glu			
180	185	190	
gcg ctg acc ctg aat acc gcc aaa ctc tgg atc cgt ttg ccg ggg cag			624
Ala Leu Thr Leu Asn Thr Ala Lys Leu Trp Ile Arg Leu Pro Gly Gln			
195	200	205	
gct gat cgc cag ccg ctg gac ggc cat ttc gcg ccg ctg ggg ttc ggg			672
Ala Asp Arg Gln Pro Leu Asp Gly His Phe Ala Pro Leu Gly Phe Gly			
210	215	220	
gag cag gat aca ctg tgg ccg aag gcc gac agt gcg ttc agt ggt tat			720
Glu Gln Asp Thr Leu Trp Pro Lys Ala Asp Ser Ala Phe Ser Gly Tyr			
225	230	235	240
cag ctc ttg ctg gag tac ttt acc ttc cgc gaa aag ttt atg ttt gtc			768
Gln Leu Leu Leu Glu Tyr Phe Thr Phe Arg Glu Lys Phe Met Phe Val			
245	250	255	
gcg ttg cag ggg ctg gat ggg atc gag ctg ccg gcg gaa ctg ccg tgg			816
Ala Leu Gln Gly Leu Asp Gly Ile Glu Leu Pro Ala Glu Leu Pro Trp			
260	265	270	
ttt gag att gat gtg gtg ctg gaa aaa cgc tgg caa cat gat ttc tcg			864
Phe Glu Ile Asp Val Val Leu Glu Lys Arg Trp Gln His Asp Phe Ser			

275	280	285	
ttc tcc gaa aag aac ctg cgc ctg cat tgt gtg ccg gtg att aac ctg			912
Phe Ser Glu Lys Asn Leu Arg Leu His Cys Val Pro Val Ile Asn Leu			
290	295	300	
ttc ccg ctg gaa tcg gac ccg ctg tca ctt tct tca tta cag acc gaa			960
Phe Pro Leu Glu Ser Asp Pro Leu Ser Leu Ser Ser Leu Gln Thr Glu			
305	310	315	320
tac ctg ctg cgc cca atg cgc att cag gac ggt tat acc gaa gtg tat			1008
Tyr Leu Leu Arg Pro Met Arg Ile Gln Asp Gly Tyr Thr Glu Val Tyr			
	325	330	335
tcg gtg gac tcg gtg atc tcc tcc cgt cat acc ggg cat cag gtc tat			1056
Ser Val Asp Ser Val Ile Ser Ser Arg His Thr Gly His Gln Val Tyr			
	340	345	350
gtc cct ttc acc agc ttt cgc cac aag ggg ggg atg ttg cgc cat gat			1104
Val Pro Phe Thr Ser Phe Arg His Lys Gly Gly Met Leu Arg His Asp			
	355	360	365
gcg ccg gag tat tac tac cat acg cgg gtc aaa cgc ggg cct tcg ggg			1152
Ala Pro Glu Tyr Tyr Tyr His Thr Arg Val Lys Arg Gly Pro Ser Gly			
	370	375	380
tta cac gat acc tgg ctg gtg ctg ggg ggc gag gcg ttt gat aac cac			1200
Leu His Asp Thr Trp Leu Val Leu Gly Gly Glu Ala Phe Asp Asn His			
	385	390	395
agc gta ccg gat aat gaa aat ttg tcg ctg agc ctg acc ggc acc aac			1248
Ser Val Pro Asp Asn Glu Asn Leu Ser Leu Ser Leu Thr Gly Thr Asn			
	405	410	415
ggg cag tta ccg cgt aaa gcg ctg caa agc acg gtg ctg gat acg gcg			1296
Gly Gln Leu Pro Arg Lys Ala Leu Gln Ser Thr Val Leu Asp Thr Ala			
	420	425	430
gtg aaa tcc acc ggg gct cag gtg cgg gtg cgt aat ctc tcc gcg ccg			1344
Val Lys Ser Thr Gly Ala Gln Val Arg Val Arg Asn Leu Ser Ala Pro			
	435	440	445
tca ttg cca tgc tac ccg ccg aac cgc gac cgt ttt cac tgg cgg gtg			1392
Ser Leu Pro Cys Tyr Pro Pro Asn Arg Asp Arg Phe His Trp Arg Val			
	450	455	460
ctg agc cat ctg ggc agt agt ttt ctg tgg atg atg gat aac gcc gaa			1440
Leu Ser His Leu Gly Ser Ser Phe Leu Trp Met Met Asp Asn Ala Glu			

465	470	475	480
gtg ctg cgc ggc acg ctg gcg ctg tat gac tgg acg gac aac gaa atg			1488
Val Leu Arg Gly Thr Leu Ala Leu Tyr Asp Trp Thr Asp Asn Glu Met			
	485	490	495
aac cgc cgt cgg ctg gag gcg atc gcc gag gtc aaa cac agc gag att			1536
Asn Arg Arg Arg Leu Glu Ala Ile Ala Glu Val Lys His Ser Glu Ile			
	500	505	510
gaa cgc ttt gag cgg ggc tat ttg ctg cgc ggg gtg cac att gaa atc			1584
Glu Arg Phe Glu Arg Gly Tyr Leu Leu Arg Gly Val His Ile Glu Ile			
	515	520	525
acc ctc gac agc aac ggc ttt acc ggt acc ggg gat att tgt ctg ttt			1632
Thr Leu Asp Ser Asn Gly Phe Thr Gly Thr Gly Asp Ile Cys Leu Phe			
	530	535	540
ggg gaa atg ctc agt cgc ttc ttt gcc ctg tat acc gat att cac ctg			1680
Gly Glu Met Leu Ser Arg Phe Phe Ala Leu Tyr Thr Asp Ile His Leu			
	545	550	555
ttt aat cgt ctg act ctg ata ctg caa ccg aca gga gaa cgt ttg gaa			1728
Phe Asn Arg Leu Thr Leu Ile Leu Gln Pro Thr Gly Glu Arg Leu Glu			
	565	570	575
tgg gaa gag aat cat cag tcc cgc ctt ccc ggc taa			1764
Trp Glu Glu Asn His Gln Ser Arg Leu Pro Gly			
	580	585	

<210> 45

<211> 587

<212> PRT

<213> Yersinia pestis

<400> 45

Met Asp Asp Leu Thr Leu Arg Tyr Phe Asp Ala Glu Met Arg Tyr Leu			
1	5	10	15
Arg Glu Ala Gly Glu Glu Phe Ala Arg Ala His Pro Asp Arg Ala Ala			
20	25	30	
Gly Leu Asn Leu Asp Lys Ala Gly Ala Arg Asp Pro Tyr Val Glu Arg			
35	40	45	
Leu Phe Glu Gly Phe Ala Phe Leu Met Gly Arg Leu Arg Glu Lys Leu			
50	55	60	

Asp Asp Asp Leu Pro Glu Leu Thr Glu Gly Leu Val Ser Leu Leu Trp
 65 70 75 80
 Pro His Tyr Leu Arg Thr Ile Pro Ser Leu Ser Ile Val Glu Phe Thr
 85 90 95
 Pro Gln Trp Gln Gly Met Lys Glu Arg Met Gly Val Ser Lys Gly Phe
 100 105 110
 Glu Val Leu Ser Arg Pro Ile Gly Glu Arg Glu Thr Arg Cys Arg Tyr
 115 120 125
 Thr Thr Thr Gln Glu Met Asp Leu Leu Pro Leu Thr Leu Arg Arg Ala
 130 135 140
 Gly Leu Asp Ser Glu Pro Asp Gly Arg Ser Val Ile Arg Leu Arg Phe
 145 150 155 160
 Asp Cys Ser Ala Leu Ala Asp Trp Ser Arg Ile Asn Leu Ser Arg Leu
 165 170 175
 Pro Leu Tyr Phe Asp Ala Asp Ala Pro Leu Ala Cys Ala Leu His Glu
 180 185 190
 Ala Leu Thr Leu Asn Thr Ala Lys Leu Trp Ile Arg Leu Pro Gly Gln
 195 200 205
 Ala Asp Arg Gln Pro Leu Asp Gly His Phe Ala Pro Leu Gly Phe Gly
 210 215 220
 Glu Gln Asp Thr Leu Trp Pro Lys Ala Asp Ser Ala Phe Ser Gly Tyr
 225 230 235 240
 Gln Leu Leu Leu Glu Tyr Phe Thr Phe Arg Glu Lys Phe Met Phe Val
 245 250 255
 Ala Leu Gln Gly Leu Asp Gly Ile Glu Leu Pro Ala Glu Leu Pro Trp
 260 265 270
 Phe Glu Ile Asp Val Val Leu Glu Lys Arg Trp Gln His Asp Phe Ser
 275 280 285
 Phe Ser Glu Lys Asn Leu Arg Leu His Cys Val Pro Val Ile Asn Leu
 290 295 300
 Phe Pro Leu Glu Ser Asp Pro Leu Ser Leu Ser Ser Leu Gln Thr Glu
 305 310 315 320

Tyr Leu Leu Arg Pro Met Arg Ile Gln Asp Gly Tyr Thr Glu Val Tyr
 325 330 335
 Ser Val Asp Ser Val Ile Ser Ser Arg His Thr Gly His Gln Val Tyr
 340 345 350
 Val Pro Phe Thr Ser Phe Arg His Lys Gly Gly Met Leu Arg His Asp
 355 360 365
 Ala Pro Glu Tyr Tyr Tyr His Thr Arg Val Lys Arg Gly Pro Ser Gly
 370 375 380
 Leu His Asp Thr Trp Leu Val Leu Gly Gly Glu Ala Phe Asp Asn His
 385 390 395 400
 Ser Val Pro Asp Asn Glu Asn Leu Ser Leu Ser Leu Thr Gly Thr Asn
 405 410 415
 Gly Gln Leu Pro Arg Lys Ala Leu Gln Ser Thr Val Leu Asp Thr Ala
 420 425 430
 Val Lys Ser Thr Gly Ala Gln Val Arg Val Arg Asn Leu Ser Ala Pro
 435 440 445
 Ser Leu Pro Cys Tyr Pro Pro Asn Arg Asp Arg Phe His Trp Arg Val
 450 455 460
 Leu Ser His Leu Gly Ser Ser Phe Leu Trp Met Met Asp Asn Ala Glu
 465 470 475 480
 Val Leu Arg Gly Thr Leu Ala Leu Tyr Asp Trp Thr Asp Asn Glu Met
 485 490 495
 Asn Arg Arg Arg Leu Glu Ala Ile Ala Glu Val Lys His Ser Glu Ile
 500 505 510
 Glu Arg Phe Glu Arg Gly Tyr Leu Leu Arg Gly Val His Ile Glu Ile
 515 520 525
 Thr Leu Asp Ser Asn Gly Phe Thr Gly Thr Gly Asp Ile Cys Leu Phe
 530 535 540
 Gly Glu Met Leu Ser Arg Phe Phe Ala Leu Tyr Thr Asp Ile His Leu
 545 550 555 560
 Phe Asn Arg Leu Thr Leu Ile Leu Gln Pro Thr Gly Glu Arg Leu Glu
 565 570 575

Trp Glu Glu Asn His Gln Ser Arg Leu Pro Gly
 580 585

<210> 46

<211> 669

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(669)

<400> 46

atg ttg tca ggt att caa tcg gca tca cta ata tgt cat tcg tct tca 48
 Met Leu Ser Gly Ile Gln Ser Ala Ser Leu Ile Cys His Ser Ser Ser
 1 5 10 15

ata gaa gaa agt gaa aaa att caa tca gtt gtt ttt tta tct gat atc 96
 Ile Glu Glu Ser Glu Lys Ile Gln Ser Val Val Phe Leu Ser Asp Ile
 20 25 30

ggt ctt gat aaa aac agg tta aca cta gag caa gaa aag gga ttg aag 144
 Gly Leu Asp Lys Asn Arg Leu Thr Leu Glu Gln Glu Lys Gly Leu Lys
 35 40 45

gat ata aaa tca tct ata gat gat tgt tat cac aac ggt att agt act 192
 Asp Ile Lys Ser Ser Ile Asp Asp Cys Tyr His Asn Gly Ile Ser Thr
 50 55 60

agt act ggc agg aaa aaa ata aaa gaa tta aga aat aaa gtt acc cag 240
 Ser Thr Gly Arg Lys Lys Ile Lys Glu Leu Arg Asn Lys Val Thr Gln
 65 70 75 80

tac att aac tct gta gag agt tac cgg gat aag att tat gat gtt atc 288
 Tyr Ile Asn Ser Val Glu Ser Tyr Arg Asp Lys Ile Tyr Asp Val Ile
 85 90 95

att gat aaa aga acg ggc aga ggt gaa aag ata ata tta aaa tct gga 336
 Ile Asp Lys Arg Thr Gly Arg Gly Glu Lys Ile Ile Leu Lys Ser Gly
 100 105 110

tgt gat gaa aca cat aga aat agt tat ctt aag ggg att att tat ctc 384
 Cys Asp Glu Thr His Arg Asn Ser Tyr Leu Lys Gly Ile Ile Tyr Leu
 115 120 125

agt aaa ttg cag gat ctt att cgt aat gaa ata gat aat gca cct att 432
 Ser Lys Leu Gln Asp Leu Ile Arg Asn Glu Ile Asp Asn Ala Pro Ile
 130 135 140

aaa tat aaa aaa tca cta agt aaa gtt ttt gat gtc atg gga aaa ggc 480
 Lys Tyr Lys Lys Ser Leu Ser Lys Val Phe Asp Val Met Gly Lys Gly
 145 150 155 160

gct gtg tat ggc gac ata aag gca ctg aat gaa gat cgt aaa ttg cct 528
 Ala Val Tyr Gly Asp Ile Lys Ala Leu Asn Glu Asp Arg Lys Leu Pro
 165 170 175

gat ttt aaa tat agt gac tct gaa tgt tct gcg tat gat tat agc tat 576
 Asp Phe Lys Tyr Ser Asp Ser Glu Cys Ser Ala Tyr Asp Tyr Ser Tyr
 180 185 190

ggc aac cat gca ctt gaa tgt ggt att cgc tct ttg gaa tgc gca gga 624
 Gly Asn His Ala Leu Glu Cys Gly Ile Arg Ser Leu Glu Cys Ala Gly
 195 200 205

cag act gga tta ctg atc tgt atg tgt cta atg gga ggg aaa tga 669
 Gln Thr Gly Leu Leu Ile Cys Met Cys Leu Met Gly Gly Lys
 210 215 220

<210> 47

<211> 222

<212> PRT

<213> Yersinia pestis

<400> 47

Met Leu Ser Gly Ile Gln Ser Ala Ser Leu Ile Cys His Ser Ser Ser
 1 5 10 15

Ile Glu Glu Ser Glu Lys Ile Gln Ser Val Val Phe Leu Ser Asp Ile
 20 25 30

Gly Leu Asp Lys Asn Arg Leu Thr Leu Glu Gln Glu Lys Gly Leu Lys
 35 40 45

Asp Ile Lys Ser Ser Ile Asp Asp Cys Tyr His Asn Gly Ile Ser Thr
 50 55 60

Ser Thr Gly Arg Lys Lys Ile Lys Glu Leu Arg Asn Lys Val Thr Gln
 65 70 75 80

Tyr Ile Asn Ser Val Glu Ser Tyr Arg Asp Lys Ile Tyr Asp Val Ile
 85 90 95

Ile Asp Lys Arg Thr Gly Arg Gly Glu Lys Ile Ile Leu Lys Ser Gly
 100 105 110

Cys Asp Glu Thr His Arg Asn Ser Tyr Leu Lys Gly Ile Ile Tyr Leu
 115 120 125

Ser Lys Leu Gln Asp Leu Ile Arg Asn Glu Ile Asp Asn Ala Pro Ile
 130 135 140

Lys Tyr Lys Lys Ser Leu Ser Lys Val Phe Asp Val Met Gly Lys Gly
 145 150 155 160

Ala Val Tyr Gly Asp Ile Lys Ala Leu Asn Glu Asp Arg Lys Leu Pro
 165 170 175

Asp Phe Lys Tyr Ser Asp Ser Glu Cys Ser Ala Tyr Asp Tyr Ser Tyr
 180 185 190

Gly Asn His Ala Leu Glu Cys Gly Ile Arg Ser Leu Glu Cys Ala Gly
 195 200 205

Gln Thr Gly Leu Leu Ile Cys Met Cys Leu Met Gly Gly Lys
 210 215 220

<210> 48

<211> 1602

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(1602)

<400> 48

atg gcg acg tta act acc ttg ctc acc gct tgt gcc gca gag cct gag 48
 Met Ala Thr Leu Thr Thr Leu Leu Thr Ala Cys Ala Ala Glu Pro Glu
 1 5 10 15

cca ctt tta cag cag gcc aga caa cag gtt gcg ctc tgg gaa cgt tgg 96
 Pro Leu Leu Gln Gln Ala Arg Gln Gln Val Ala Leu Trp Glu Arg Trp
 20 25 30

ttg caa ccg gtg aca ccc gat aag cat acc ggt gaa gac ccc ggt tac 144
 Leu Gln Pro Val Thr Pro Asp Lys His Thr Gly Glu Asp Pro Gly Tyr
 35 40 45

gat gac cac ttc caa cag atg cgt gaa gag gtc aat aag ctc tcg ggt	192
Asp Asp His Phe Gln Gln Met Arg Glu Glu Val Asn Lys Leu Ser Gly	
50 55 60	
gcc gat acc acg ctg acc tgc gag ctg gct gaa aag ctg ttc acc aca	240
Ala Asp Thr Thr Leu Thr Cys Glu Leu Ala Glu Lys Leu Phe Thr Thr	
65 70 75 80	
cac ggc aag gat gtg cgg gtg gca acc tat tac gtc tgg gcg cgg ttg	288
His Gly Lys Asp Val Arg Val Ala Thr Tyr Tyr Val Trp Ala Arg Leu	
85 90 95	
cac cgt gac ggc gag gcc ggg ctg gcg gat ggc ctt tcc ctg ctg gcc	336
His Arg Asp Gly Glu Ala Gly Leu Ala Asp Gly Leu Ser Leu Leu Ala	
100 105 110	
ggg ctg atc acg cgc ttt ggt gag ggc ctg cat ccg ctg cgt aca acc	384
Gly Leu Ile Thr Arg Phe Gly Glu Gly Leu His Pro Leu Arg Thr Thr	
115 120 125	
agc cgg aaa acc gcg ttg gag tgg ctg gcc ggc tcc cgg atg cgc gac	432
Ser Arg Lys Thr Ala Leu Glu Trp Leu Ala Gly Ser Arg Met Arg Asp	
130 135 140	
agc ttg tca ctt tac ccg gaa gtg gat aaa gcc gat ttt gag cgt atc	480
Ser Leu Ser Leu Tyr Pro Glu Val Asp Lys Ala Asp Phe Glu Arg Ile	
145 150 155 160	
gtg ggc gca ctg gcc ctt atc gaa cag agg ctc agt ctc tgg gac gaa	528
Val Gly Ala Leu Ala Leu Ile Glu Gln Arg Leu Ser Leu Trp Asp Glu	
165 170 175	
ggc gtc cgg ccg caa ctg ggc ggg ttg tat acc gcc ctg gaa aac cgc	576
Gly Val Arg Pro Gln Leu Gly Gly Leu Tyr Thr Ala Leu Glu Asn Arg	
180 185 190	
ctc gcg caa tct ggt ggg cta aat gcc gtg gtg ccg caa aac agc agc	624
Leu Ala Gln Ser Gly Gly Leu Asn Ala Val Val Pro Gln Asn Ser Ser	
195 200 205	
ggg tca tca tcg gca ggc agc ttg aac cca gcc aac acg gcg tca ccg	672
Gly Ser Ser Ser Ala Gly Ser Leu Asn Pro Ala Asn Thr Ala Ser Pro	
210 215 220	
gcg ttg cgg cca gtg caa tcg gga cgt gac ctg ctc gat cag acc aaa	720
Ala Leu Arg Pro Val Gln Ser Gly Arg Asp Leu Leu Asp Gln Thr Lys	
225 230 235 240	

acg ctg gca aaa tac ctg cgc aac cag ccg cag ggc tgg ctc tcc ggg 768
 Thr Leu Ala Lys Tyr Leu Arg Asn Gln Pro Gln Gly Trp Leu Ser Gly
 245 250 255

cat cat ctt atc aaa agc gtg cgc tgg gat acg gta cat cag tca ccg 816
 His His Leu Ile Lys Ser Val Arg Trp Asp Thr Val His Gln Ser Pro
 260 265 270

cca tta gat gtg aac gga cgg acc cgg ctg gta ccg ccg cgc ccg gaa 864
 Pro Leu Asp Val Asn Gly Arg Thr Arg Leu Val Pro Pro Arg Pro Glu
 275 280 285

tat cgc gta caa ctc aag cgc ctt tat ctg caa caa aac tgg ctg gcg 912
 Tyr Arg Val Gln Leu Lys Arg Leu Tyr Leu Gln Gln Asn Trp Leu Ala
 290 295 300

ttg ctg gaa cag gcc gaa tcg ata ttt gcc gaa ggg gtt aac cat ttc 960
 Leu Leu Glu Gln Ala Glu Ser Ile Phe Ala Glu Gly Val Asn His Phe
 305 310 315 320

tgg ctc gat gtg cag tgg tat ctg cat cag gcc ctc agc aaa gcg ggg 1008
 Trp Leu Asp Val Gln Trp Tyr Leu His Gln Ala Leu Ser Lys Ala Gly
 325 330 335

gcc cca ttc gat ggc tgg gcg agc tgt atc acg cag gat tta cgg tta 1056
 Ala Pro Phe Asp Gly Trp Ala Ser Cys Ile Thr Gln Asp Leu Arg Leu
 340 345 350

tta ctg acc cgg ctg ccg ggg ctg gaa ggg cta tgc tgg agt gac ggc 1104
 Leu Leu Thr Arg Leu Pro Gly Leu Glu Gly Leu Cys Trp Ser Asp Gly
 355 360 365

acg cca ttt gcc gat gag gtg acg ctg ggg tgg ata aac cag cag gta 1152
 Thr Pro Phe Ala Asp Glu Val Thr Leu Gly Trp Ile Asn Gln Gln Val
 370 375 380

ctg gag tcg gtc tcg ggc tgg ggc agc gag ccg gcc gcc gtt tca tcc 1200
 Leu Glu Ser Val Ser Gly Trp Gly Ser Glu Pro Ala Ala Val Ser Ser
 385 390 395 400

ggt gag gat ggc att ctg ttg ctg gag cca gaa gct ttg gct cag gcg 1248
 Gly Glu Asp Gly Ile Leu Leu Leu Glu Pro Glu Ala Leu Ala Gln Ala
 405 410 415

gac agc gaa gga att gaa gcg gcg ctt aac tgg ttg cag tca cga ccg 1296
 Asp Ser Glu Gly Ile Glu Ala Ala Leu Asn Trp Leu Gln Ser Arg Pro
 420 425 430

ggg atc acc acg gcg cgc cat cag tgg ctg ctg cgt ctg gtg atg gcc 1344
 Gly Ile Thr Thr Ala Arg His Gln Trp Leu Leu Arg Leu Val Met Ala
 435 440 445

cgg gtg gcg gag cag tac ggt aag aac gat atg gcc ttg cat ctg ctg 1392
 Arg Val Ala Glu Gln Tyr Gly Lys Asn Asp Met Ala Leu His Leu Leu
 450 455 460

agt ggc ctt gat agc agc ggc gcg ttg ttg acc ttg cca cag tgg gag 1440
 Ser Gly Leu Asp Ser Ser Gly Ala Leu Leu Thr Leu Pro Gln Trp Glu
 465 470 475 480

ccg ggg ttg gtg ttt gaa gtt aaa gcc cgc cgt ttg aag ctg ttg cgt 1488
 Pro Gly Leu Val Phe Glu Val Lys Ala Arg Arg Leu Lys Leu Leu Arg
 485 490 495

atg aag gca cag cgg ggt gac agt gat aaa acc cgc ctg cat gct gaa 1536
 Met Lys Ala Gln Arg Gly Asp Ser Asp Lys Thr Arg Leu His Ala Glu
 500 505 510

atg gaa agc ctg ctc agt ggg ctt atc gcc ctc gac ccg gcc cgt gcg 1584
 Met Glu Ser Leu Leu Ser Gly Leu Ile Ala Leu Asp Pro Ala Arg Ala
 515 520 525

gcc gta tta tgc gga taa 1602
 Ala Val Leu Cys Gly
 530

<210> 49

<211> 533

<212> PRT

<213> Yersinia pestis

<400> 49

Met Ala Thr Leu Thr Thr Leu Leu Thr Ala Cys Ala Ala Glu Pro Glu
 1 5 10 15

Pro Leu Leu Gln Gln Ala Arg Gln Gln Val Ala Leu Trp Glu Arg Trp
 20 25 30

Leu Gln Pro Val Thr Pro Asp Lys His Thr Gly Glu Asp Pro Gly Tyr
 35 40 45

Asp Asp His Phe Gln Gln Met Arg Glu Glu Val Asn Lys Leu Ser Gly
 50 55 60

Ala Asp Thr Thr Leu Thr Cys Glu Leu Ala Glu Lys Leu Phe Thr Thr
 65 70 75 80
 His Gly Lys Asp Val Arg Val Ala Thr Tyr Tyr Val Trp Ala Arg Leu
 85 90 95
 His Arg Asp Gly Glu Ala Gly Leu Ala Asp Gly Leu Ser Leu Leu Ala
 100 105 110
 Gly Leu Ile Thr Arg Phe Gly Glu Gly Leu His Pro Leu Arg Thr Thr
 115 120 125
 Ser Arg Lys Thr Ala Leu Glu Trp Leu Ala Gly Ser Arg Met Arg Asp
 130 135 140
 Ser Leu Ser Leu Tyr Pro Glu Val Asp Lys Ala Asp Phe Glu Arg Ile
 145 150 155 160
 Val Gly Ala Leu Ala Leu Ile Glu Gln Arg Leu Ser Leu Trp Asp Glu
 165 170 175
 Gly Val Arg Pro Gln Leu Gly Gly Leu Tyr Thr Ala Leu Glu Asn Arg
 180 185 190
 Leu Ala Gln Ser Gly Gly Leu Asn Ala Val Val Pro Gln Asn Ser Ser
 195 200 205
 Gly Ser Ser Ser Ala Gly Ser Leu Asn Pro Ala Asn Thr Ala Ser Pro
 210 215 220
 Ala Leu Arg Pro Val Gln Ser Gly Arg Asp Leu Leu Asp Gln Thr Lys
 225 230 235 240
 Thr Leu Ala Lys Tyr Leu Arg Asn Gln Pro Gln Gly Trp Leu Ser Gly
 245 250 255
 His His Leu Ile Lys Ser Val Arg Trp Asp Thr Val His Gln Ser Pro
 260 265 270
 Pro Leu Asp Val Asn Gly Arg Thr Arg Leu Val Pro Pro Arg Pro Glu
 275 280 285
 Tyr Arg Val Gln Leu Lys Arg Leu Tyr Leu Gln Gln Asn Trp Leu Ala
 290 295 300
 Leu Leu Glu Gln Ala Glu Ser Ile Phe Ala Glu Gly Val Asn His Phe
 305 310 315 320

Trp Leu Asp Val Gln Trp Tyr Leu His Gln Ala Leu Ser Lys Ala Gly
 325 330 335
 Ala Pro Phe Asp Gly Trp Ala Ser Cys Ile Thr Gln Asp Leu Arg Leu
 340 345 350
 Leu Leu Thr Arg Leu Pro Gly Leu Glu Gly Leu Cys Trp Ser Asp Gly
 355 360 365
 Thr Pro Phe Ala Asp Glu Val Thr Leu Gly Trp Ile Asn Gln Gln Val
 370 375 380
 Leu Glu Ser Val Ser Gly Trp Gly Ser Glu Pro Ala Ala Val Ser Ser
 385 390 395 400
 Gly Glu Asp Gly Ile Leu Leu Leu Glu Pro Glu Ala Leu Ala Gln Ala
 405 410 415
 Asp Ser Glu Gly Ile Glu Ala Ala Leu Asn Trp Leu Gln Ser Arg Pro
 420 425 430
 Gly Ile Thr Thr Ala Arg His Gln Trp Leu Leu Arg Leu Val Met Ala
 435 440 445
 Arg Val Ala Glu Gln Tyr Gly Lys Asn Asp Met Ala Leu His Leu Leu
 450 455 460
 Ser Gly Leu Asp Ser Ser Gly Ala Leu Leu Thr Leu Pro Gln Trp Glu
 465 470 475 480
 Pro Gly Leu Val Phe Glu Val Lys Ala Arg Arg Leu Lys Leu Leu Arg
 485 490 495
 Met Lys Ala Gln Arg Gly Asp Ser Asp Lys Thr Arg Leu His Ala Glu
 500 505 510
 Met Glu Ser Leu Leu Ser Gly Leu Ile Ala Leu Asp Pro Ala Arg Ala
 515 520 525
 Ala Val Leu Cys Gly
 530

<210> 50

<211> 2448

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(2448)

<400> 50

atg att atc aga ttc cgg cta ccg cca tta tcg gta ctg ata tat ggc 48
 Met Ile Ile Arg Phe Arg Leu Pro Pro Leu Ser Val Leu Ile Tyr Gly
 1 5 10 15

tca ata ttg tta ccg tca ctg ata ccc ttg act att tta gga ggg agc 96
 Ser Ile Leu Leu Pro Ser Leu Ile Pro Leu Thr Ile Leu Gly Gly Ser
 20 25 30

ctc cct ccg ccc tcg aca tca aca acg atg cct gat act acg tta tat 144
 Leu Pro Pro Pro Ser Thr Ser Thr Thr Met Pro Asp Thr Thr Leu Tyr
 35 40 45

ctt gaa ctc gtg gtc aat gac cgt aac ttt ggg agt act gta cct att 192
 Leu Glu Leu Val Val Asn Asp Arg Asn Phe Gly Ser Thr Val Pro Ile
 50 55 60

agt tac cgc aac aac cgt tat tac ctt tct caa tca cag cta aga acg 240
 Ser Tyr Arg Asn Asn Arg Tyr Tyr Leu Ser Gln Ser Gln Leu Arg Thr
 65 70 75 80

att ggg ctt cct ata tca gag cca ctg gca ccc gag att gcc att gat 288
 Ile Gly Leu Pro Ile Ser Glu Pro Leu Ala Pro Glu Ile Ala Ile Asp
 85 90 95

aat atg gcg ggc gtg aac gtt aaa tat gat gga gag aac caa cgc cta 336
 Asn Met Ala Gly Val Asn Val Lys Tyr Asp Gly Glu Asn Gln Arg Leu
 100 105 110

tta atc aat gtt ccc agc gag tgg cta cca aag caa caa atc gag gtt 384
 Leu Ile Asn Val Pro Ser Glu Trp Leu Pro Lys Gln Gln Ile Glu Val
 115 120 125

acc gaa caa gat gat ttc aat ctt gcg caa agt agt ttg ggg gct tta 432
 Thr Glu Gln Asp Asp Phe Asn Leu Ala Gln Ser Ser Leu Gly Ala Leu
 130 135 140

ttc aat tac gat atc tat gcc aca caa ggt tac ccg tac tca tct tta 480
 Phe Asn Tyr Asp Ile Tyr Ala Thr Gln Gly Tyr Pro Tyr Ser Ser Leu
 145 150 155 160

act cat ttt tca gca tgg aca gaa cag cgc att ttt gat cgt ttt ggc 528
 Thr His Phe Ser Ala Trp Thr Glu Gln Arg Ile Phe Asp Arg Phe Gly

165	170	175	
ttg ctc agt aat acc ggc gtt tat cgc acc cac ttc cca agt aat aac			576
Leu Leu Ser Asn Thr Gly Val Tyr Arg Thr His Phe Pro Ser Asn Asn			
180	185	190	
aac aca gat gac gcg aaa ggc tat att cgt ttt gat acc cag tgg cag			624
Asn Thr Asp Asp Ala Lys Gly Tyr Ile Arg Phe Asp Thr Gln Trp Gln			
195	200	205	
aag aat gac gaa gaa cat ctg ctg cgt tat agc aca ggt gac ctc att			672
Lys Asn Asp Glu Glu His Leu Leu Arg Tyr Ser Thr Gly Asp Leu Ile			
210	215	220	
acc ggt gct ttg cca tgg agc agt gcg ata cgt ctt ggc ggc att cag			720
Thr Gly Ala Leu Pro Trp Ser Ser Ala Ile Arg Leu Gly Gly Ile Gln			
225	230	235	240
ata gca cgg cat ttt gct att cgg ccc gat ctc ata acc tac cca tta			768
Ile Ala Arg His Phe Ala Ile Arg Pro Asp Leu Ile Thr Tyr Pro Leu			
245	250	255	
cca caa ttt tct ggt cag gcc gca gtc ccc agc acc gtt gat ctc tac			816
Pro Gln Phe Ser Gly Gln Ala Ala Val Pro Ser Thr Val Asp Leu Tyr			
260	265	270	
att gat aac ttc agg aca caa tcg gcc aat atc aac cca ggc cct ttt			864
Ile Asp Asn Phe Arg Thr Gln Ser Ala Asn Ile Asn Pro Gly Pro Phe			
275	280	285	
gtc atc aat aat gca ccg cga atc aat ggt gca ggc caa gcg act atc			912
Val Ile Asn Asn Ala Pro Arg Ile Asn Gly Ala Gly Gln Ala Thr Ile			
290	295	300	
gtc aca acc gat gcc ctt ggc agg caa atc agc aca tct gta ccc ttt			960
Val Thr Thr Asp Ala Leu Gly Arg Gln Ile Ser Thr Ser Val Pro Phe			
305	310	315	320
tac gtt gcc agt aca ctg cta aaa ccc gga gtg tgg gat ttc agt ctc			1008
Tyr Val Ala Ser Thr Leu Leu Lys Pro Gly Val Trp Asp Phe Ser Leu			
325	330	335	
tcg ggg ggt gcc cta cgt cgt aat tat gcg att cgc tca gca gat tac			1056
Ser Gly Gly Ala Leu Arg Arg Asn Tyr Ala Ile Arg Ser Ala Asp Tyr			
340	345	350	
ggt gaa atg gtt gcc agt ggt gtc gtt cgt tac ggc aca aca cct tgg			1104
Gly Glu Met Val Ala Ser Gly Val Val Arg Tyr Gly Thr Thr Pro Trp			

355	360	365	
ttg aca ctg gag ggc cgg gga gac atc gcc aaa gaa atg cat gta att			1152
Leu Thr Leu Glu Gly Arg Gly Asp Ile Ala Lys Glu Met His Val Ile			
370	375	380	
ggg ggt ggc gtt aat ttt cgc atg ggg tta ttg ggt gtc cta aat agt			1200
Gly Gly Gly Val Asn Phe Arg Met Gly Leu Leu Gly Val Leu Asn Ser			
385	390	395	400
gca tac agt ata agc aac aca tcg aac ggc gct ttt aac aat gtg gct			1248
Ala Tyr Ser Ile Ser Asn Thr Ser Asn Gly Ala Phe Asn Asn Val Ala			
405	410	415	
gaa ccg cta aat acc aat aat gcc acg ccg aat aga tta ccg tcc cca			1296
Glu Pro Leu Asn Thr Asn Asn Ala Thr Pro Asn Arg Leu Pro Ser Pro			
420	425	430	
gca gcg tca cgc cgt gga cgt ggc aac cag cgt tca tta ggc tat agc			1344
Ala Ala Ser Arg Arg Gly Arg Gly Asn Gln Arg Ser Leu Gly Tyr Ser			
435	440	445	
tac agt aat gca ttc ttt aat tta aat gct caa cat att atc tct agt			1392
Tyr Ser Asn Ala Phe Phe Asn Leu Asn Ala Gln His Ile Ile Ser Ser			
450	455	460	
gat gaa tac agt gac ctt gcc aat tat aaa acg cct tct ctc tta agc			1440
Asp Glu Tyr Ser Asp Leu Ala Asn Tyr Lys Thr Pro Ser Leu Leu Ser			
465	470	475	480
cga cgc atg act caa ctc acg gga agt ctc agc ctc ggt agt tac ggc			1488
Arg Arg Met Thr Gln Leu Thr Gly Ser Leu Ser Leu Gly Ser Tyr Gly			
485	490	495	
acc gtg gga tcg ggt tac ttt gat gtc agg gat gct ctt ggc gaa caa			1536
Thr Val Gly Ser Gly Tyr Phe Asp Val Arg Asp Ala Leu Gly Glu Gln			
500	505	510	
acc cgg ctc att aat atc agc tac agc acc tca ctg tta cgc aat agc			1584
Thr Arg Leu Ile Asn Ile Ser Tyr Ser Thr Ser Leu Leu Arg Asn Ser			
515	520	525	
aac ttt tat agc gca cta aac cgt gag ctg ggc cgt aaa ggt tac aat			1632
Asn Phe Tyr Ser Ala Leu Asn Arg Glu Leu Gly Arg Lys Gly Tyr Asn			
530	535	540	
gta caa ctg gtc tgg agc att ccg tta ggc ccg cgg gga tca agc agc			1680
Val Gln Leu Val Trp Ser Ile Pro Leu Gly Pro Arg Gly Ser Ser Ser			

545	550	555	560	
atc agt gca acc cgc aca aat gat aac caa tgg att caa caa ctg aat				1728
Ile Ser Ala Thr Arg Thr Asn Asp Asn Gln Trp Ile Gln Gln Leu Asn				
	565	570	575	
tat agc cgt tca gcg ccc tcg aat ggg gga ttg ggc tgg aac ctc gct				1776
Tyr Ser Arg Ser Ala Pro Ser Asn Gly Gly Leu Gly Trp Asn Leu Ala				
	580	585	590	
tat gcc aac agc acg aat aac aat aat caa tac caa cag gca gac att				1824
Tyr Ala Asn Ser Thr Asn Asn Asn Asn Gln Tyr Gln Gln Ala Asp Ile				
	595	600	605	
gtt tgg cgt act tca atg atg gag agt cgc atg ggc cta tat ggt aac				1872
Val Trp Arg Thr Ser Met Met Glu Ser Arg Met Gly Leu Tyr Gly Asn				
	610	615	620	
agt aat aac tac aac tat tgg ggg gga tta acc ggt tca tta gtg gtg				1920
Ser Asn Asn Tyr Asn Tyr Trp Gly Gly Leu Thr Gly Ser Leu Val Val				
	625	630	635	640
atg aat agg agt gtc tat gcc agc aat atg att aac gat gct ttt gct				1968
Met Asn Arg Ser Val Tyr Ala Ser Asn Met Ile Asn Asp Ala Phe Ala				
	645	650	655	
ttg gta tcg acc aat ggt ttt agt aat att ccg gtt agt tac gaa aat				2016
Leu Val Ser Thr Asn Gly Phe Ser Asn Ile Pro Val Ser Tyr Glu Asn				
	660	665	670	
caa ctt att ggc aca act aat gcc aag ggt tat ttg ctg atc ccg aca				2064
Gln Leu Ile Gly Thr Thr Asn Ala Lys Gly Tyr Leu Leu Ile Pro Thr				
	675	680	685	
gtc gcc tca tat tat cag gca aaa ttc cag att gac cca atg aat tta				2112
Val Ala Ser Tyr Tyr Gln Ala Lys Phe Gln Ile Asp Pro Met Asn Leu				
	690	695	700	
ccg gca gat gtc atg cta ccc aat gtt gaa cgg cgg tta gcc att ggt				2160
Pro Ala Asp Val Met Leu Pro Asn Val Glu Arg Arg Leu Ala Ile Gly				
	705	710	715	720
gaa cgc agt ggc tat tta att aat ttc ccc att aag cga att tcc gca				2208
Glu Arg Ser Gly Tyr Leu Ile Asn Phe Pro Ile Lys Arg Ile Ser Ala				
	725	730	735	
gtg aat att aga att aca gac gca tca ggc caa gac tta ccg aaa ggc				2256
Val Asn Ile Arg Ile Thr Asp Ala Ser Gly Gln Asp Leu Pro Lys Gly				

740	745	750	
agt gca ata tat act acc ggt aac atc ccc ata agt tat gtc ggt tgg			2304
Ser Ala Ile Tyr Thr Thr Gly Asn Ile Pro Ile Ser Tyr Val Gly Trp			
755	760	765	
gat ggc atg gta tat atc gag caa gtg gca caa tta aat aac ctt agg			2352
Asp Gly Met Val Tyr Ile Glu Gln Val Ala Gln Leu Asn Asn Leu Arg			
770	775	780	
att ata .cgt gcc gat aat ggc aca cag tgc tac agc cag ttc aaa cta			2400
Ile Ile Arg Ala Asp Asn Gly Thr Gln Cys Tyr Ser Gln Phe Lys Leu			
785	790	795	800
aag acg acg gaa ggt ata cag gat gct ggc acc aca gta tgc cga tag			2448
Lys Thr Thr Glu Gly Ile Gln Asp Ala Gly Thr Thr Val Cys Arg			
805	810	815	

<210> 51

<211> 815

<212> PRT

<213> Yersinia pestis

<400> 51

Met Ile Ile Arg Phe Arg Leu Pro Pro Leu Ser Val Leu Ile Tyr Gly
1 5 10 15

Ser Ile Leu Leu Pro Ser Leu Ile Pro Leu Thr Ile Leu Gly Gly Ser
20 25 30

Leu Pro Pro Pro Ser Thr Ser Thr Thr Met Pro Asp Thr Thr Leu Tyr
35 40 45

Leu Glu Leu Val Val Asn Asp Arg Asn Phe Gly Ser Thr Val Pro Ile
50 55 60

Ser Tyr Arg Asn Asn Arg Tyr Tyr Leu Ser Gln Ser Gln Leu Arg Thr
65 70 75 80

Ile Gly Leu Pro Ile Ser Glu Pro Leu Ala Pro Glu Ile Ala Ile Asp
85 90 95

Asn Met Ala Gly Val Asn Val Lys Tyr Asp Gly Glu Asn Gln Arg Leu
100 105 110

Leu Ile Asn Val Pro Ser Glu Trp Leu Pro Lys Gln Gln Ile Glu Val
115 120 125

Thr Glu Gln Asp Asp Phe Asn Leu Ala Gln Ser Ser Leu Gly Ala Leu
 130 135 140
 Phe Asn Tyr Asp Ile Tyr Ala Thr Gln Gly Tyr Pro Tyr Ser Ser Leu
 145 150 155 160
 Thr His Phe Ser Ala Trp Thr Glu Gln Arg Ile Phe Asp Arg Phe Gly
 165 170 175
 Leu Leu Ser Asn Thr Gly Val Tyr Arg Thr His Phe Pro Ser Asn Asn
 180 185 190
 Asn Thr Asp Asp Ala Lys Gly Tyr Ile Arg Phe Asp Thr Gln Trp Gln
 195 200 205
 Lys Asn Asp Glu Glu His Leu Leu Arg Tyr Ser Thr Gly Asp Leu Ile
 210 215 220
 Thr Gly Ala Leu Pro Trp Ser Ser Ala Ile Arg Leu Gly Gly Ile Gln
 225 230 235 240
 Ile Ala Arg His Phe Ala Ile Arg Pro Asp Leu Ile Thr Tyr Pro Leu
 245 250 255
 Pro Gln Phe Ser Gly Gln Ala Ala Val Pro Ser Thr Val Asp Leu Tyr
 260 265 270
 Ile Asp Asn Phe Arg Thr Gln Ser Ala Asn Ile Asn Pro Gly Pro Phe
 275 280 285
 Val Ile Asn Asn Ala Pro Arg Ile Asn Gly Ala Gly Gln Ala Thr Ile
 290 295 300
 Val Thr Thr Asp Ala Leu Gly Arg Gln Ile Ser Thr Ser Val Pro Phe
 305 310 315 320
 Tyr Val Ala Ser Thr Leu Leu Lys Pro Gly Val Trp Asp Phe Ser Leu
 325 330 335
 Ser Gly Gly Ala Leu Arg Arg Asn Tyr Ala Ile Arg Ser Ala Asp Tyr
 340 345 350
 Gly Glu Met Val Ala Ser Gly Val Val Arg Tyr Gly Thr Thr Pro Trp
 355 360 365
 Leu Thr Leu Glu Gly Arg Gly Asp Ile Ala Lys Glu Met His Val Ile
 370 375 380

Gly Gly Gly Val Asn Phe Arg Met Gly Leu Leu Gly Val Leu Asn Ser
 385 390 395 400

Ala Tyr Ser Ile Ser Asn Thr Ser Asn Gly Ala Phe Asn Asn Val Ala
 405 410 415

Glu Pro Leu Asn Thr Asn Asn Ala Thr Pro Asn Arg Leu Pro Ser Pro
 420 425 430

Ala Ala Ser Arg Arg Gly Arg Gly Asn Gln Arg Ser Leu Gly Tyr Ser
 435 440 445

Tyr Ser Asn Ala Phe Phe Asn Leu Asn Ala Gln His Ile Ile Ser Ser
 450 455 460

Asp Glu Tyr Ser Asp Leu Ala Asn Tyr Lys Thr Pro Ser Leu Leu Ser
 465 470 475 480

Arg Arg Met Thr Gln Leu Thr Gly Ser Leu Ser Leu Gly Ser Tyr Gly
 485 490 495

Thr Val Gly Ser Gly Tyr Phe Asp Val Arg Asp Ala Leu Gly Glu Gln
 500 505 510

Thr Arg Leu Ile Asn Ile Ser Tyr Ser Thr Ser Leu Leu Arg Asn Ser
 515 520 525

Asn Phe Tyr Ser Ala Leu Asn Arg Glu Leu Gly Arg Lys Gly Tyr Asn
 530 535 540

Val Gln Leu Val Trp Ser Ile Pro Leu Gly Pro Arg Gly Ser Ser Ser
 545 550 555 560

Ile Ser Ala Thr Arg Thr Asn Asp Asn Gln Trp Ile Gln Gln Leu Asn
 565 570 575

Tyr Ser Arg Ser Ala Pro Ser Asn Gly Gly Leu Gly Trp Asn Leu Ala
 580 585 590

Tyr Ala Asn Ser Thr Asn Asn Asn Asn Gln Tyr Gln Gln Ala Asp Ile
 595 600 605

Val Trp Arg Thr Ser Met Met Glu Ser Arg Met Gly Leu Tyr Gly Asn
 610 615 620

Ser Asn Asn Tyr Asn Tyr Trp Gly Gly Leu Thr Gly Ser Leu Val Val
 625 630 635 640

Met Asn Arg Ser Val Tyr Ala Ser Asn Met Ile Asn Asp Ala Phe Ala
 645 650 655

Leu Val Ser Thr Asn Gly Phe Ser Asn Ile Pro Val Ser Tyr Glu Asn
 660 665 670

Gln Leu Ile Gly Thr Thr Asn Ala Lys Gly Tyr Leu Leu Ile Pro Thr
 675 680 685

Val Ala Ser Tyr Tyr Gln Ala Lys Phe Gln Ile Asp Pro Met Asn Leu
 690 695 700

Pro Ala Asp Val Met Leu Pro Asn Val Glu Arg Arg Leu Ala Ile Gly
 705 710 715 720

Glu Arg Ser Gly Tyr Leu Ile Asn Phe Pro Ile Lys Arg Ile Ser Ala
 725 730 735

Val Asn Ile Arg Ile Thr Asp Ala Ser Gly Gln Asp Leu Pro Lys Gly
 740 745 750

Ser Ala Ile Tyr Thr Thr Gly Asn Ile Pro Ile Ser Tyr Val Gly Trp
 755 760 765

Asp Gly Met Val Tyr Ile Glu Gln Val Ala Gln Leu Asn Asn Leu Arg
 770 775 780

Ile Ile Arg Ala Asp Asn Gly Thr Gln Cys Tyr Ser Gln Phe Lys Leu
 785 790 795 800

Lys Thr Thr Glu Gly Ile Gln Asp Ala Gly Thr Thr Val Cys Arg
 805 810 815

<210> 52

<211> 1233

<212> DNA

<213> Yersinia pestis

<220>

<221> CDS

<222> (1)..(1233)

<400> 52

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Met Glu Ile Val Asn Phe Ile Ser Ala Gln Asp Ile Val Glu Ile Glu

1	5	10	15	
ttt ctc tca aca gag aat gaa aaa aat aaa gag gca ttg aat tca gta				96
Phe Leu Ser Thr Glu Asn Glu Lys Asn Lys Glu Ala Leu Asn Ser Val				
	20	25	30	
aat aaa tgg gag aat gat gct cca ttt ggg gaa aac aga acc aat gct				144
Asn Lys Trp Glu Asn Asp Ala Pro Phe Gly Glu Asn Arg Thr Asn Ala				
	35	40	45	
gct aat gaa att cgt gat gtt ata gag aga aat gcg cct ata ctt agg				192
Ala Asn Glu Ile Arg Asp Val Ile Glu Arg Asn Ala Pro Ile Leu Arg				
	50	55	60	
cta tcg cgt ctg aat atc agt tct tta cct gat gtt tta ccg cat agt				240
Leu Ser Arg Leu Asn Ile Ser Ser Leu Pro Asp Val Leu Pro His Ser				
	65	70	75	80
ctc atc gag att gaa att tat tat tgc gat gaa tta tct act ctc cct				288
Leu Ile Glu Ile Glu Ile Tyr Tyr Cys Asp Glu Leu Ser Thr Leu Pro				
	85	90	95	
gac agt ttt cct tcc gag ctt act aag cta aaa att agc cat tgc cct				336
Asp Ser Phe Pro Ser Glu Leu Thr Lys Leu Lys Ile Ser His Cys Pro				
	100	105	110	
gaa att tca tct tta tat aag aat gca cca aag cgt ttg act aaa tta				384
Glu Ile Ser Ser Leu Tyr Lys Asn Ala Pro Lys Arg Leu Thr Lys Leu				
	115	120	125	
gaa ata ata tct tgt ccg aaa att tca aat gct ata att cca ctg cct				432
Glu Ile Ile Ser Cys Pro Lys Ile Ser Asn Ala Ile Ile Pro Leu Pro				
	130	135	140	
gaa tca tta caa tat att aaa tta gat ata gac tcg aaa gag cgc ctt				480
Glu Ser Leu Gln Tyr Ile Lys Leu Asp Ile Asp Ser Lys Glu Arg Leu				
	145	150	155	160
tct ctc tcg ttt gat aaa ttt cct aaa aat tta aga ggt att aat tta				528
Ser Leu Ser Phe Asp Lys Phe Pro Lys Asn Leu Arg Gly Ile Asn Leu				
	165	170	175	
agt gat agt ttt tta att gaa aaa agc aaa ttc aag gat aga gag atc				576
Ser Asp Ser Phe Leu Ile Glu Lys Ser Lys Phe Lys Asp Arg Glu Ile				
	180	185	190	
cga ttg aat gtt cta gtg cca tcc gta gct cta gag ttt aaa tta ggg				624
Arg Leu Asn Val Leu Val Pro Ser Val Ala Leu Glu Phe Lys Leu Gly				

195	200	205	
gac att cta tat gga att gct cag tgt caa cat gag gtg atg cag caa			672
Asp Ile Leu Tyr Gly Ile Ala Gln Cys Gln His Glu Val Met Gln Gln			
210	215	220	
cta att aat ttt aat gac ttt tct aac aaa gat att tgt tcg caa aca			720
Leu Ile Asn Phe Asn Asp Phe Ser Asn Lys Asp Ile Cys Ser Gln Thr			
225	230	235	240
aca att act gat gct gtt tgg gaa cat cgt aat tat ttt tcc cgt gat			768
Thr Ile Thr Asp Ala Val Trp Glu His Arg Asn Tyr Phe Ser Arg Asp			
245	250	255	
aaa tat aga gac gat gcg aca atc aaa gaa atg tta aat gat gct gat			816
Lys Tyr Arg Asp Asp Ala Thr Ile Lys Glu Met Leu Asn Asp Ala Asp			
260	265	270	
cgc gga att aaa ttc aaa gat ttc cta gaa aaa cat gaa aag tat aat			864
Arg Gly Ile Lys Phe Lys Asp Phe Leu Glu Lys His Glu Lys Tyr Asn			
275	280	285	
att tta agt cgt tcg gga ata aaa tca tac cgt cct cat aaa aat gag			912
Ile Leu Ser Arg Ser Gly Ile Lys Ser Tyr Arg Pro His Lys Asn Glu			
290	295	300	
gag gat ata tgt tta tca agg acc agt aag gct ggt ctt gaa ttt cag			960
Glu Asp Ile Cys Leu Ser Arg Thr Ser Lys Ala Gly Leu Glu Phe Gln			
305	310	315	320
atc atg gaa agg caa gag cgt gta ttt ttt tgt ata gat aat ttg aat			1008
Ile Met Glu Arg Gln Glu Arg Val Phe Phe Cys Ile Asp Asn Leu Asn			
325	330	335	
aat tgt att cct gaa att gca caa aaa aaa cct gat tat ggt acc tat			1056
Asn Cys Ile Pro Glu Ile Ala Gln Lys Lys Pro Asp Tyr Gly Thr Tyr			
340	345	350	
atc aca gcc tct gag ttg aga tgg ctt tac cgt cgt aaa gat cac cct			1104
Ile Thr Ala Ser Glu Leu Arg Trp Leu Tyr Arg Arg Lys Asp His Pro			
355	360	365	
aat gta aaa aat aat gtt caa ttc tgc ttg gag gga gca ttt att tca			1152
Asn Val Lys Asn Asn Val Gln Phe Cys Leu Glu Gly Ala Phe Ile Ser			
370	375	380	
caa gaa gag gta ttt tca ctg cct ggt tgg gaa act tat ttt cct aaa			1200
Gln Glu Glu Val Phe Ser Leu Pro Gly Trp Glu Thr Tyr Phe Pro Lys			

385 390 395 400

aga aaa agt aac ttc ata cct tcc tat gtt tga 1233

Arg Lys Ser Asn Phe Ile Pro Ser Tyr Val

 405 410

<210> 53

<211> 410

<212> PRT

<213> Yersinia pestis

<400> 53

Met Glu Ile Val Asn Phe Ile Ser Ala Gln Asp Ile Val Glu Ile Glu

1 5 10 15

Phe Leu Ser Thr Glu Asn Glu Lys Asn Lys Glu Ala Leu Asn Ser Val

 20 25 30

Asn Lys Trp Glu Asn Asp Ala Pro Phe Gly Glu Asn Arg Thr Asn Ala

 35 40 45

Ala Asn Glu Ile Arg Asp Val Ile Glu Arg Asn Ala Pro Ile Leu Arg

 50 55 60

Leu Ser Arg Leu Asn Ile Ser Ser Leu Pro Asp Val Leu Pro His Ser

65 70 75 80

Leu Ile Glu Ile Glu Ile Tyr Tyr Cys Asp Glu Leu Ser Thr Leu Pro

 85 90 95

Asp Ser Phe Pro Ser Glu Leu Thr Lys Leu Lys Ile Ser His Cys Pro

 100 105 110

Glu Ile Ser Ser Leu Tyr Lys Asn Ala Pro Lys Arg Leu Thr Lys Leu

 115 120 125

Glu Ile Ile Ser Cys Pro Lys Ile Ser Asn Ala Ile Ile Pro Leu Pro

 130 135 140

Glu Ser Leu Gln Tyr Ile Lys Leu Asp Ile Asp Ser Lys Glu Arg Leu

145 150 155 160

Ser Leu Ser Phe Asp Lys Phe Pro Lys Asn Leu Arg Gly Ile Asn Leu

 165 170 175

Ser Asp Ser Phe Leu Ile Glu Lys Ser Lys Phe Lys Asp Arg Glu Ile

 180 185 190

Arg Leu Asn Val Leu Val Pro Ser Val Ala Leu Glu Phe Lys Leu Gly
 195 200 205

Asp Ile Leu Tyr Gly Ile Ala Gln Cys Gln His Glu Val Met Gln Gln
 210 215 220

Leu Ile Asn Phe Asn Asp Phe Ser Asn Lys Asp Ile Cys Ser Gln Thr
 225 230 235 240

Thr Ile Thr Asp Ala Val Trp Glu His Arg Asn Tyr Phe Ser Arg Asp
 245 250 255

Lys Tyr Arg Asp Asp Ala Thr Ile Lys Glu Met Leu Asn Asp Ala Asp
 260 265 270

Arg Gly Ile Lys Phe Lys Asp Phe Leu Glu Lys His Glu Lys Tyr Asn
 275 280 285

Ile Leu Ser Arg Ser Gly Ile Lys Ser Tyr Arg Pro His Lys Asn Glu
 290 295 300

Glu Asp Ile Cys Leu Ser Arg Thr Ser Lys Ala Gly Leu Glu Phe Gln
 305 310 315 320

Ile Met Glu Arg Gln Glu Arg Val Phe Phe Cys Ile Asp Asn Leu Asn
 325 330 335

Asn Cys Ile Pro Glu Ile Ala Gln Lys Lys Pro Asp Tyr Gly Thr Tyr
 340 345 350

Ile Thr Ala Ser Glu Leu Arg Trp Leu Tyr Arg Arg Lys Asp His Pro
 355 360 365

Asn Val Lys Asn Asn Val Gln Phe Cys Leu Glu Gly Ala Phe Ile Ser
 370 375 380

Gln Glu Glu Val Phe Ser Leu Pro Gly Trp Glu Thr Tyr Phe Pro Lys
 385 390 395 400

Arg Lys Ser Asn Phe Ile Pro Ser Tyr Val
 405 410

<210> 54

<211> 2082

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1) .. (2082)

<400> 54

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Met	Lys	Gly	Arg	Leu	Leu	Asp	Ala	Val	Pro	Leu	Ser	Thr	Leu	Ser	Gly	
1				5				10						15		

ggt	ggc	gca	agt	cag	gct	gga	aaa	ctc	gcc	aag	ata	ggt	ttg	gaa	acc	96
Val	Gly	Ala	Ser	Gln	Ala	Gly	Lys	Leu	Ala	Lys	Ile	Gly	Leu	Glu	Thr	
		20						25						30		

att	cag	gac	ctg	ctg	ctg	cac	ctt	ccg	cta	cgt	tat	gag	gat	cgt	act	144
Ile	Gln	Asp	Leu	Leu	Leu	His	Leu	Pro	Leu	Arg	Tyr	Glu	Asp	Arg	Thr	
		35					40					45				

cgt	cta	tat	cgt	att	ggt	gat	ctg	ctg	ccc	ggt	ctt	tcg	gtc	acg	gtt	192
Arg	Leu	Tyr	Arg	Ile	Gly	Asp	Leu	Leu	Pro	Gly	Leu	Ser	Val	Thr	Val	
	50					55					60					

gaa	ggt	gaa	gtt	cta	cgc	tct	gat	att	agc	ttt	ggt	cgc	cgc	cgt	atg	240
Glu	Gly	Glu	Val	Leu	Arg	Ser	Asp	Ile	Ser	Phe	Gly	Arg	Arg	Arg	Met	
65					70					75					80	

atg	acc	tgt	caa	atc	agc	gat	ggt	agc	ggc	gtt	ctc	acc	ctg	cgc	ttt	288
Met	Thr	Cys	Gln	Ile	Ser	Asp	Gly	Ser	Gly	Val	Leu	Thr	Leu	Arg	Phe	
			85						90					95		

ttt	aac	ttc	aat	gca	gca	atg	aaa	aac	agt	ctg	tca	gta	ggc	aaa	cat	336
Phe	Asn	Phe	Asn	Ala	Ala	Met	Lys	Asn	Ser	Leu	Ser	Val	Gly	Lys	His	
			100					105					110			

gtc	att	gct	tat	ggc	gaa	gcc	aaa	cga	ggc	aat	aac	ggg	cca	gaa	atc	384
Val	Ile	Ala	Tyr	Gly	Glu	Ala	Lys	Arg	Gly	Asn	Asn	Gly	Pro	Glu	Ile	
		115					120					125				

att	cac	cct	gaa	tat	cgg	gtt	cat	ggc	gag	aat	att	ggc	gtt	gaa	tta	432
Ile	His	Pro	Glu	Tyr	Arg	Val	His	Gly	Glu	Asn	Ile	Gly	Val	Glu	Leu	
		130				135					140					

cag	gaa	tcg	ctg	aca	cca	gtc	tat	ccc	acg	acc	gag	ggc	att	cgt	cag	480
Gln	Glu	Ser	Leu	Thr	Pro	Val	Tyr	Pro	Thr	Thr	Glu	Gly	Ile	Arg	Gln	
145					150					155				160		

gca	act	ctg	cgc	aaa	ctt	atc	gat	cag	gca	ctg	gca	atg	ctg	gac	acc	528
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Ala Thr Leu Arg Lys Leu Ile Asp Gln Ala Leu Ala Met Leu Asp Thr	
165 170 175	
tgt gtt att gct gag tta ctg cca att gaa ttg agc cgt tct ctc atc	576
Cys Val Ile Ala Glu Leu Leu Pro Ile Glu Leu Ser Arg Ser Leu Ile	
180 185 190	
agc ctg cct gaa gcg att cat act ctg cat cgc cct ccg gca gat att	624
Ser Leu Pro Glu Ala Ile His Thr Leu His Arg Pro Pro Ala Asp Ile	
195 200 205	
caa tta gct gat tta gaa caa ggg aag cac ccc gct caa cgg cgt ctg	672
Gln Leu Ala Asp Leu Glu Gln Gly Lys His Pro Ala Gln Arg Arg Leu	
210 215 220	
atc atg gaa gag ttg ctg gct cat aac ctc agt atg ttg gca gtc agg	720
Ile Met Glu Glu Leu Leu Ala His Asn Leu Ser Met Leu Ala Val Arg	
225 230 235 240	
gcg ggt gca caa agc tac cga gca ttg cca tta atg gcc gaa gag cag	768
Ala Gly Ala Gln Ser Tyr Arg Ala Leu Pro Leu Met Ala Glu Glu Gln	
245 250 255	
ctt aaa caa cgt ttt ctg gcc gcc cta cct ttt acg cct act caa gcc	816
Leu Lys Gln Arg Phe Leu Ala Ala Leu Pro Phe Thr Pro Thr Gln Ala	
260 265 270	
cag caa cgg gtc gtc gcc gaa att gaa cgg gat atg acc caa agt ttc	864
Gln Gln Arg Val Val Ala Glu Ile Glu Arg Asp Met Thr Gln Ser Phe	
275 280 285	
ccg atg atg cga ctg att cag ggg gat gta ggt tcc ggt aaa aca ctg	912
Pro Met Met Arg Leu Ile Gln Gly Asp Val Gly Ser Gly Lys Thr Leu	
290 295 300	
gta gcc gca ctg gcc gcg cta cgg gcc atc gct cac ggt aag cag gtt	960
Val Ala Ala Leu Ala Ala Leu Arg Ala Ile Ala His Gly Lys Gln Val	
305 310 315 320	
gcc ctg atg gca ccg acc gaa ctg ctg gca gaa cag cac gcc act act	1008
Ala Leu Met Ala Pro Thr Glu Leu Leu Ala Glu Gln His Ala Thr Thr	
325 330 335	
ttc cgt caa tgg ctg gag cct ctt ggg ttt agt gtc ggc tgg ttg gct	1056
Phe Arg Gln Trp Leu Glu Pro Leu Gly Phe Ser Val Gly Trp Leu Ala	
340 345 350	
ggc aag caa aag ggg aaa gcg cgg tta gca caa caa gag gcc gtt gcc	1104

Gly Lys Gln Lys Gly Lys Ala Arg Leu Ala Gln Gln Glu Ala Val Ala	
355 360 365	
agc ggt cag gtc tcc atg gtg atc ggt act cat gcc atg ttt caa gaa	1152
Ser Gly Gln Val Ser Met Val Ile Gly Thr His Ala Met Phe Gln Glu	
370 375 380	
cag gtg caa ttc tcg ggg tta gca ctg gta att att gat gag cag cat	1200
Gln Val Gln Phe Ser Gly Leu Ala Leu Val Ile Ile Asp Glu Gln His	
385 390 395 400	
cgt ttc ggt gtt cac cag cgc ctc acg tta tgg gaa aaa ggt gag gag	1248
Arg Phe Gly Val His Gln Arg Leu Thr Leu Trp Glu Lys Gly Glu Glu	
405 410 415	
caa ggc ttc cat cca cat caa tta atc atg acg gca acc ccg atc cca	1296
Gln Gly Phe His Pro His Gln Leu Ile Met Thr Ala Thr Pro Ile Pro	
420 425 430	
aga aca tta gcc atg act gcc tat gca gat ctc gat acc tcc gtg att	1344
Arg Thr Leu Ala Met Thr Ala Tyr Ala Asp Leu Asp Thr Ser Val Ile	
435 440 445	
gat gaa tta ccg cca ggc aga acc ccc gtg aca acg gtg gca atc ccg	1392
Asp Glu Leu Pro Pro Gly Arg Thr Pro Val Thr Thr Val Ala Ile Pro	
450 455 460	
gat act cgc cgt agt gat gtt att cag cgg gtt aaa aac gcg tgc ctg	1440
Asp Thr Arg Arg Ser Asp Val Ile Gln Arg Val Lys Asn Ala Cys Leu	
465 470 475 480	
gaa gag ggt agg caa gca tat tgg gta tgt acc ttg att gaa gaa tca	1488
Glu Glu Gly Arg Gln Ala Tyr Trp Val Cys Thr Leu Ile Glu Glu Ser	
485 490 495	
gag ttg ctg gag gct cag gct gca gag gta acg tgc gaa gag ctg aaa	1536
Glu Leu Leu Glu Ala Gln Ala Ala Glu Val Thr Cys Glu Glu Leu Lys	
500 505 510	
att gcc tta ccg gaa att aaa gtt ggc ttg gtt cat ggg cgg atg aaa	1584
Ile Ala Leu Pro Glu Ile Lys Val Gly Leu Val His Gly Arg Met Lys	
515 520 525	
ggc ccc gaa aaa cag gcg att atg ctg gcc ttt aaa caa ggt gag cta	1632
Gly Pro Glu Lys Gln Ala Ile Met Leu Ala Phe Lys Gln Gly Glu Leu	
530 535 540	
cag tta ttg gtc gca acc acg gtg att gaa gtg gga gtt gat gtg ccc	1680

Gln Leu Leu Val Ala Thr Thr Val Ile Glu Val Gly Val Asp Val Pro
 545 550 555 560

 aat gcc agc ttg atg att atc gat aat cct gaa cgg ttg ggg ctg gcg 1728
 Asn Ala Ser Leu Met Ile Ile Asp Asn Pro Glu Arg Leu Gly Leu Ala
 565 570 575

 cag tta cat cag tta cgt ggg cgt gtc ggg cgc ggt gct gtc gct tcc 1776
 Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
 580 585 590

 cac tgc gta tta ctc tat aaa acg cca tta agt aaa acc gct caa atg 1824
 His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Met
 595 600 605

 cgg ttg cag gta tta cgt gat agc aat gat ggt ttt gtg att gca cag 1872
 Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
 610 615 620

 cga gat cta gaa atc cgt ggc ccc ggt gag cta ttg ggc aca cgg caa 1920
 Arg Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
 625 630 635 640

 aca ggt agc gca gag ttt aag gtt gcc gac cta ctt cgt gat caa gcg 1968
 Thr Gly Ser Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
 645 650 655

 atg atc cca gaa gtt cag cgg gtc gcc cgt cat ctg cat caa cag tac 2016
 Met Ile Pro Glu Val Gln Arg Val Ala Arg His Leu His Gln Gln Tyr
 660 665 670

 cct gaa cat gcc aag gca ttg ata gaa cgc tgg ttg ccg gag cgg gta 2064
 Pro Glu His Ala Lys Ala Leu Ile Glu Arg Trp Leu Pro Glu Arg Val
 675 680 685

 cgg tat acc aat gcg taa 2082
 Arg Tyr Thr Asn Ala
 690

<210> 55

<211> 693

<212> PRT

<213> Yersinia pestis

<400> 55

Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Thr Leu Ser Gly

1

5

10

15

Val Gly Ala Ser Gln Ala Gly Lys Leu Ala Lys Ile Gly Leu Glu Thr
 20 25 30
 Ile Gln Asp Leu Leu Leu His Leu Pro Leu Arg Tyr Glu Asp Arg Thr
 35 40 45
 Arg Leu Tyr Arg Ile Gly Asp Leu Leu Pro Gly Leu Ser Val Thr Val
 50 55 60
 Glu Gly Glu Val Leu Arg Ser Asp Ile Ser Phe Gly Arg Arg Arg Met
 65 70 75 80
 Met Thr Cys Gln Ile Ser Asp Gly Ser Gly Val Leu Thr Leu Arg Phe
 85 90 95
 Phe Asn Phe Asn Ala Ala Met Lys Asn Ser Leu Ser Val Gly Lys His
 100 105 110
 Val Ile Ala Tyr Gly Glu Ala Lys Arg Gly Asn Asn Gly Pro Glu Ile
 115 120 125
 Ile His Pro Glu Tyr Arg Val His Gly Glu Asn Ile Gly Val Glu Leu
 130 135 140
 Gln Glu Ser Leu Thr Pro Val Tyr Pro Thr Thr Glu Gly Ile Arg Gln
 145 150 155 160
 Ala Thr Leu Arg Lys Leu Ile Asp Gln Ala Leu Ala Met Leu Asp Thr
 165 170 175
 Cys Val Ile Ala Glu Leu Leu Pro Ile Glu Leu Ser Arg Ser Leu Ile
 180 185 190
 Ser Leu Pro Glu Ala Ile His Thr Leu His Arg Pro Pro Ala Asp Ile
 195 200 205
 Gln Leu Ala Asp Leu Glu Gln Gly Lys His Pro Ala Gln Arg Arg Leu
 210 215 220
 Ile Met Glu Glu Leu Leu Ala His Asn Leu Ser Met Leu Ala Val Arg
 225 230 235 240
 Ala Gly Ala Gln Ser Tyr Arg Ala Leu Pro Leu Met Ala Glu Glu Gln
 245 250 255
 Leu Lys Gln Arg Phe Leu Ala Ala Leu Pro Phe Thr Pro Thr Gln Ala
 260 265 270

Gln Gln Arg Val Val Ala Glu Ile Glu Arg Asp Met Thr Gln Ser Phe
 275 280 285
 Pro Met Met Arg Leu Ile Gln Gly Asp Val Gly Ser Gly Lys Thr Leu
 290 295 300
 Val Ala Ala Leu Ala Ala Leu Arg Ala Ile Ala His Gly Lys Gln Val
 305 310 315 320
 Ala Leu Met Ala Pro Thr Glu Leu Leu Ala Glu Gln His Ala Thr Thr
 325 330 335
 Phe Arg Gln Trp Leu Glu Pro Leu Gly Phe Ser Val Gly Trp Leu Ala
 340 345 350
 Gly Lys Gln Lys Gly Lys Ala Arg Leu Ala Gln Gln Glu Ala Val Ala
 355 360 365
 Ser Gly Gln Val Ser Met Val Ile Gly Thr His Ala Met Phe Gln Glu
 370 375 380
 Gln Val Gln Phe Ser Gly Leu Ala Leu Val Ile Ile Asp Glu Gln His
 385 390 395 400
 Arg Phe Gly Val His Gln Arg Leu Thr Leu Trp Glu Lys Gly Glu Glu
 405 410 415
 Gln Gly Phe His Pro His Gln Leu Ile Met Thr Ala Thr Pro Ile Pro
 420 425 430
 Arg Thr Leu Ala Met Thr Ala Tyr Ala Asp Leu Asp Thr Ser Val Ile
 435 440 445
 Asp Glu Leu Pro Pro Gly Arg Thr Pro Val Thr Thr Val Ala Ile Pro
 450 455 460
 Asp Thr Arg Arg Ser Asp Val Ile Gln Arg Val Lys Asn Ala Cys Leu
 465 470 475 480
 Glu Glu Gly Arg Gln Ala Tyr Trp Val Cys Thr Leu Ile Glu Glu Ser
 485 490 495
 Glu Leu Leu Glu Ala Gln Ala Ala Glu Val Thr Cys Glu Glu Leu Lys
 500 505 510
 Ile Ala Leu Pro Glu Ile Lys Val Gly Leu Val His Gly Arg Met Lys
 515 520 525

Gly Pro Glu Lys Gln Ala Ile Met Leu Ala Phe Lys Gln Gly Glu Leu
 530 535 540

Gln Leu Leu Val Ala Thr Thr Val Ile Glu Val Gly Val Asp Val Pro
 545 550 555 560

Asn Ala Ser Leu Met Ile Ile Asp Asn Pro Glu Arg Leu Gly Leu Ala
 565 570 575

Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
 580 585 590

His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Met
 595 600 605

Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
 610 615 620

Arg Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
 625 630 635 640

Thr Gly Ser Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
 645 650 655

Met Ile Pro Glu Val Gln Arg Val Ala Arg His Leu His Gln Gln Tyr
 660 665 670

Pro Glu His Ala Lys Ala Leu Ile Glu Arg Trp Leu Pro Glu Arg Val
 675 680 685

Arg Tyr Thr Asn Ala
 690

<210> 56

<211> 1220

<212> DNA

<213> Yersinia pestis

<400> 56

atgaacagtg aaaaaaaga acatcttaat acagtatcaa gaaagttaag aacgatcatg 60
 gagcgtgata atattgatgc tgtcattgtg acaacgtgtg ataattttta tcatgttacc 120
 ggtattctca gtttttttat gtataccttt cgaatacggg caccgctatc gccgttgtct 180
 tccgtgatgt gaaaattcca tcgctaataa ttatgaatga atttgaagca gccagcttaa 240
 cggttgatat gccaaatgct gaattaaaga cctttcctgt ttgggtagat gtagatgatc 300
 cgtttaacat ggcgcattct gcaaataata ataaagagag gccgataggt cctcctattg 360

```

agagtgtatg taatatactc aaagacgcat tgaacgatgc caggggtactt aataaaaaaa 420
tagcaataga cctcaatata atgtcaaacg gtggtaaaag agttattgat gccgttatgc 480
ctaattgtga ttttgtcgac tcaagctcta tattcaacga gctaagagtg ataaaaagcc 540
cttgggaaat taaaagactc agaaaaagtg cagaaattac ggaaatatggg atcactgaag 600
catcaaagct catccgggta ggatgcacat cagctgaact cactgccgca tataaggcag 660
cagtaatgag taaatctgaa actcactttt caagattcca tcttatctct gttggcgctg 720
atttttcacc caaactcata ccaagcaata ctaaagcctg ttcaggcgac ttaattaaat 780
ttgattgcgg cgctgatgtt gatggttatg gtgccgatat tgccaggact tttgttggtg 840
gggaacctcc cgagatcacc cggaagatat accaaacaat aagaactggg catgaacata 900
tgctgagtat ggttgcgcct ggcgtaaaaa tgaaagatgt atttgattca acgatggagg 960
tcattaaaaa gtccgggtta cctaattata acagagggca tcttgggcat ggtaatggcg 1020
tctttttggg attagaagag agtcccttcg ttagcactca tgctacagaa tcgttcactt 1080
caggtatggt gctaagttta gaaacacctt actacggcta taatttgggt tcgattatga 1140
ttgaagatat gattttaata aataaagagg gtattgagtt tttgagtaaa ttaccagggg 1200
atttagtttc ttttaattaa
1220

```

<210> 57

<211> 965

<212> DNA

<213> *Yersinia pestis*

<400> 57

```

atggataaga aacgcgtatt tattgccggg catcgtggca tgggtgggttc tgctattgta 60
cgtcaacttg aaaaccgtaa tgatattgag ttgatcatta gggatcgta tgaacttgac 120
ctcatgtctc aatccgctgt gcaaaaattt tttgctactg aaaaaattga tgaaatctat 180
ttggctgcgg caaaagtggg gggattcagg ccaataataa ttatccggca gagttcatct 240
accaaaactt aatgatcgag tgcaatatta ttcacgcggc tcatttagct ggcattcaaa 300
aattattatt tttgggtct tcttgtattt atccaaaatt ggctgcacaa ccaatgacag 360
aggaggtctt gttaactggc gtcttgaac caacgaatga accttatgcc atcgccaaga 420
tagccggtat caaactgtgc gaatcttata atcgtcaata tggtcgcgat tatcgagtg 480
ttatgccaac caacctttat ggtgaaaatg acaattttca ccccgaaaat tcccatgtca 540
ttcctgcctt attacgtcgc ttccatgagg ctaaaattcg taatgataag gaaatggttg 600
tgtggggaac gggtaaacca atgcgtgagt tcctgcatgt agatgatatg gctgctgcca 660
gtgtgcatgt catggagctg tctgatcaaa tttatcaaac caatactcaa ccaatgcttt 720
cgcatattaa tgtcggaacg ggtgtggatt gcactattcg tgaattggca gaaactatgg 780
ctaaagtgtg tggtttcacc ggaaatttag tttttgattc aactaagccg gacggaacac 840
cacgaaaatt gatggacgta agccgcttgg ctaaactcgg gtgggtgttat cagatttcgc 900
ttgaagtagg tttaacgatg acttatcaat ggttcttggc tcatcagaat aacttcagaa 960
aatag
965

```

<210> 58

<211> 1076

<212> DNA

<213> *Yersinia pestis*

<400> 58

```

atgattaata atagtttctg gcaaggtaaa cgggtttttg taacaggcca tactgggttt 60
aaaggtggct ggttgagttt atggttgcaa accatggggg caacggtaaa aggttactct 120
ttgccccccc cccacaggtg cctagcctat ttgagaccgc acgagttgcc gacgggatgc 180
aatcggaat cggatgatatt cgtgatcaaa acaaattatt agaatcaatc cgcgaattcc 240
aaccagagat tgtttccac atggctgctc agccactggt ccgtctatcc tattccgagc 300
ctgttgaaac ctactcgacg aatgttatgg gtaccgttta ttactggaa gctattcgcc 360
atgttggtgg cgtcaaagcg gtggtcaata tcaccagtga taaatgctac gataataaag 420
agtggatctg gggctatcgc gaaaatgaag cgatgggggg gtatgatcct tactccaaca 480
gtaaagggtg tgcggaatta gtgacgtcat cctaccgtaa ttcgttcttc aatccagcga 540
actatggcca gcatggcact gccgtagcga cagtgcgtgc gggtaatgtt atcgggtgtg 600
gcatgtgggc attggatcgc atcgttccag atattcttcg ggcgtttgaa cagtcccaac 660
cagtattat tcgcaaccca catgccattc gcccatggca gcatgtgttg gagcctttgt 720
cgggttattt gctgttgga cagaagttat atactgacgg tgctgaatat gccgaaggtt 780
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tgaaatattg gggagagggg gcaagctggc aattagatgg caatgctcac cctcatgaag 900
ctcattatct gaaactggat tgttcaaaag ctaaaatgca acttggctgg catcctcgct 960
ggaacttgaa tactacgctc gaatatattg tgggctggca caagaactgg ttatcaggca 1020
cagatatgca tgaatacagt attactgaaa ttaataatta catgaacact aaatga 1076

```

<210> 59

<211> 220

<212> DNA

<213> *Yersinia pseudotuberculosis*

<400> 59

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gtgctgaagc aacgcagaga agacaaagaa tacaatacca aaaatcttca ttaaaacgct 60
atatgttatt atctcactag gttttaaaac ttgggacatt actatgtaat cagtctgaat 120
aataattgta gttaaaatag aaaaaattag aaaccagag gcacgacgga caataggctt 180
aataatatca gatctaattc tacgaagctt gcatgcctgc 220

```

<210> 60

<211> 265

<212> DNA

<213> *Yersinia pseudotuberculosis*

<400> 60

```

ttcgccgagg gatatcactc cgcaaatacc accggcatag agacaatctc gccacgcctt 60
gccgtctttt agcgttacga gagcggccag gcagatcgaa gcgccgacac cgtaaatagt 120
gtgcccgctc caccagcggg ataaataatt tcagcaagat cgctatcaac ataatcccaa 180
cccctgcgcc aaatggctta caggatttgt gggggcaagc gtggtttctg gataaaggcc 240
agcggctagg ccgaattcga gctcg 265

```

<210> 61

<211> 571

<212> DNA

<213> *Yersinia pseudotuberculosis*

<400> 61

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tcaataaggt gtacgcgcct gagttggaaa ttgaagtaaa aaactaacac aacgggttacg 60
ggcaattgac aataattcta ttgaacaatt tcttattctg cgtcgtcatt atctgccgca 120
tgaaaatgac gatatagaaa gtctggcccg tgccgtttgg ttagataacc gttattggga 180
taatacccggt atttctattg ccaatggaat tggctctggca tttaaaggcg attaataaaa 240
agtctcgatt ttaccttaag catgattgat aaaatcacac ggccattaaa atccgtgcaa 300
gcctctgtaa aaggatttgc ggaaagtctt caggcggtt tcggtaaaaat tgccattggc 360
ggggccgcgc tgttcggtgt cgtacagga atgaaggcg cactgggacc cgcagctgaa 420
tttgccggcg cgcttaatga ggccagcgcc aaggcgctga gtgattgcgc cttgcaaaaag 480
atgagcgctg acgccctgaa attcagtatg caatatggcc gcagcgccgt gggatgttgt 540
gcgttcaaat gcagacatgg cgcaagtga a 571
```

<210> 62

<211> 423

<212> DNA

<213> *Yersinia pseudotuberculosis*

<400> 62

```
aagccacagt tatcttgatg tggacattat gcattgtaat agcccattaa catgcgctaa 60
gaagcataaa ttaatatata gtaacaagca ttacgaggtg ctaatgtttg gaaagcagcc 120
tcttccaact acaataataa gttaactatc ctccaccac aaataattac aaatgacccc 180
tttccgctat aactccgac tcaccagcgg ctgcgtacaa acccgagagt gtcgcattat 240
tactggcttg ttactccaag agcttgatga agctgcctgg gataaagcca tgtataagga 300
aaatgtgctt cagaaacgca cgcaatctac ggtaagacgt atttcttcag cgcttagaaa 360
acgcctagaa cacctaagct ctgacttttg ggcttttgcg tttttatgct aggccgaatt 420
cga 423
```

<210> 63

<211> 380

<212> DNA

<213> *Yersinia pseudotuberculosis*

<400> 63

```
gctgagtagc ctgatatttt tatggtgaaa aagataaaca atcatagagg ggataaatat 60
gagccagttc taccattggt cagataagtt taagcaagat actgtcaatc acagtgacca 120
ttcatggtca ttacacttcc tccagttgcc agacaatgcc taacataaaa acgcaaaagc 180
ccaaaagtca gagcttaggt gttctaggcc taatccaagc tcggaagaaa tacgtcttac 240
cgtaaattgc gtgcgtttct gaagcacatt ttccttatac atggctttat cccaggcagc 300
ttcatcaagc tcttgagta acaagccagt aataatgcga cactctcggg tttgtagcga 360
gccgctggtg agatcggagt 380
```

<210> 64

<211> 243

<212> DNA

<213> *Yersinia pestis*

<220>

<221> CDS

<222> (1)..(243)

<400> 64

atg gaa aca aga ttc cta cag gca aac aaa gaa gca cgc tgg gcc ttc 48
 Met Glu Thr Arg Phe Leu Gln Ala Asn Lys Glu Ala Arg Trp Ala Phe
 1 5 10 15

ggc tta aca ctg gcc tac ctc gca ggg tgg att ata acc gct tac tta 96
 Gly Leu Thr Leu Ala Tyr Leu Ala Gly Trp Ile Ile Thr Ala Tyr Leu
 20 25 30

ccg ggc aac ctt ccc gga atg agc ggc cta cct gct tgg ttt gaa gcg 144
 Pro Gly Asn Leu Pro Gly Met Ser Gly Leu Pro Ala Trp Phe Glu Ala
 35 40 45

gcc tgt atc gca tta ccg ctc ctg ttt att gtg ctg tgt att ctg atg 192
 Ala Cys Ile Ala Leu Pro Leu Leu Phe Ile Val Leu Cys Ile Leu Met
 50 55 60

gtg cgg ctg ata ttc cgc gat att cca ctg gag gat gac gat gca aac 240
 Val Arg Leu Ile Phe Arg Asp Ile Pro Leu Glu Asp Asp Asp Ala Asn
 65 70 75 80

tga 243

<210> 65

<211> 80

<212> PRT

<213> *Yersinia pestis*

<400> 65

Met Glu Thr Arg Phe Leu Gln Ala Asn Lys Glu Ala Arg Trp Ala Phe
 1 5 10 15

Gly Leu Thr Leu Ala Tyr Leu Ala Gly Trp Ile Ile Thr Ala Tyr Leu
 20 25 30

Pro Gly Asn Leu Pro Gly Met Ser Gly Leu Pro Ala Trp Phe Glu Ala
 35 40 45

Ala Cys Ile Ala Leu Pro Leu Leu Phe Ile Val Leu Cys Ile Leu Met

50

55

60

Val Arg Leu Ile Phe Arg Asp Ile Pro Leu Glu Asp Asp Asp Ala Asn
65 70 75 80